

167257

STIC-Biotech/ChemLib

From: Yu, Misook
Sent: Thursday, September 29, 2005 9:19 AM
To: STIC-Biotech/ChemLib
Subject: 09/670,568

Pls do Interference search only for SEQ ID NO:2, and DNA encoding SEQ ID NO:1

Examiner Misook Yu, Ph.D.
571-272-0839 (Phone)
Art Unit 1642
REM-3A18 (Room)
REM-3C18 (Mail Box)

RECEIVED
SEP 29 2005
STIC/BIOTECH DIVISION
(STIC)

Searcher: Gar
Searcher Phone: 22504
Date Searcher Picked up: 10/3/05
Date completed: 10/3/05
Searcher Prep Time: 6
Online Time: 10

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: ☒ _____
WWW/Internet: _____
Other (Specify): _____

Db 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGGTGGCAGAAAACAAGATTGAGATT 300
Qy 301 AGCATGAGCTGTATCCGATCAGACGATCGGACCTGAGTGACCCCATGTGGCCACAGTAC 360
Db 301 AGCATGAGCTGTATCCGATCAGACGATCGGACCTGAGTGACCCCATGTGGCCACAGTAC 360
Qy 361 ACGAACCTGGGGCTCCTGAAACAGCATGACAGCAGAGATTTCAGAACGGCTCCTCGTCCACC 420
Db 361 ACGAACCTGGGGCTCCTGAAACAGCATGACAGCAGAGATTTCAGAACGGCTCCTCGTCCACC 420
Qy 421 AGTCCTTATAACAGACACCGGAGAAACAGCGTCACGGGCGCCTCGCCCTACGACAG 480
Db 421 AGTCCTTATAACAGACACCGGAGAAACAGCGTCACGGGCGCCTCGCCCTACGACAG 480
Qy 481 CCCAGCTCCACTTCGATGCTCTCTCCATCACCGGCATCCCTCCAAACAGCAGCTAC 540
Db 481 CCCAGCTCCACTTCGATGCTCTCTCCATCACCGGCATCCCTCCAAACAGCAGCTAC 540
Qy 541 CCAGGCCCGCACAGTTCGAGCTGTCTTCAGCAGTCGAGCACCGCCNAAGTCGGCCACC 600
Db 541 CCAGGCCCGCACAGTTCGAGCTGTCTTCAGCAGTCGAGCACCGCCNAAGTCGGCCACC 600
Qy 601 TGGACGTATTCCAATGAAGAACTCTACTGCGCAATTCGAAGAGACATGCCCCCATC 660
Db 601 TGGACGTATTCCAATGAAGAACTCTACTGCGCAATTCGAAGAGACATGCCCCCATC 660
Qy 661 CAGATCAAGGTGATGACCCCACTCTCAGGGAGCTGTATCCGGCGCATGCCCTGTCTAC 720
Db 661 CAGATCAAGGTGATGACCCCACTCTCAGGGAGCTGTATCCGGCGCATGCCCTGTCTAC 720
Qy 721 AAAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGGTGCCCCCAACCATGAGTCAGCCGT 780
Db 721 AAAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGGTGCCCCCAACCATGAGTCAGCCGT 780
Qy 781 GAATTCACAGGGACAGATTGCCCTCCTAGTCAATTTGATTTCGAGTAGAGGGGAAACAGC 840
Db 781 GAATTCACAGGGACAGATTGCCCTCCTAGTCAATTTGATTTCGAGTAGAGGGGAAACAGC 840
Qy 841 CATGCCAGTATGTAGAGATGCCATCACAGGAGACAGAGTGCTGGTACCTTTATGAG 900
Db 841 CATGCCAGTATGTAGAGATGCCATCACAGGAGACAGAGTGCTGGTACCTTTATGAG 900
Qy 901 CCAGCCAGGTGGCACTGAATTCACGACAGCTCTGTACAAATTCATGTGTAAACAGCAGT 960
Db 901 CCAGCCAGGTGGCACTGAATTCACGACAGCTCTGTACAAATTCATGTGTAAACAGCAGT 960
Qy 961 TGTGTTGAGGGATGAACCGCCGTCCAAATTTTAATCATTTGTTACTCTGGAACCCAGAGAT 1020
Db 961 TGTGTTGAGGGATGAACCGCCGTCCAAATTTTAATCATTTGTTACTCTGGAACCCAGAGAT 1020
Qy 1021 GGGCAAGTCTGGGCCAGCCTGCTTTGAGCCCGGATCTGTGCTTCCCGAGGAGAGAC 1080
Db 1021 GGGCAAGTCTGGGCCAGCCTGCTTTGAGCCCGGATCTGTGCTTCCCGAGGAGAGAC 1080
Qy 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAAACGGT 1140
Db 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAAACGGT 1140
Qy 1141 GATGGTACGAAGCGCCGTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
Db 1141 GATGGTACGAAGCGCCGTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
Qy 1201 AAACGAGATCCCGAGATGAACTGTATCTTACCATGAGGGCGCGTGAGACTTAT 1260
Db 1201 AAACGAGATCCCGAGATGAACTGTATCTTACCATGAGGGCGCGTGAGACTTAT 1260
Qy 1261 GAAATGCTGTGAAGATCAAGAGTCCCTGGAACCTCATGAGTACCTTCTCAGCACACA 1320
Db 1261 GAAATGCTGTGAAGATCAAGAGTCCCTGGAACCTCATGAGTACCTTCTCAGCACACA 1320
Qy 1321 ATTGAAACGTACGGCAACAGCAACAGCAGCAGCACTTACTTTCAGAAACATCTC 1380

Db 1321 ATTGAAACGTACGGCAACAGCAACAGCAGCAGCACCTTACTTCTAGAAACATCTC 1380
Qy 1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGAGCCCGGAGAGAAATCTCCAAAACAATCT 1440
Db 1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGAGCCCGGAGAGAAATCTCCAAAACAATCT 1440
Qy 1441 GAGCTCTCTTTAGACATTCGAAGCCCCCAACCGGATCAGTGTAACCATAGAGCCCTATC 1500
Db 1441 GAGCTCTCTTTAGACATTCGAAGCCCCCAACCGGATCAGTGTAACCATAGAGCCCTATC 1500
Qy 1501 TCTATATTTTAAAGTGTGTGTTTATTCATGTGTATATGTGAGTGTGTGTGTGTA 1560
Db 1501 TCTATATTTTAAAGTGTGTGTTTATTCATGTGTATATGTGAGTGTGTGTGTGTA 1560
Qy 1561 TGTGTGTGCGTGTATCTAGCCCTCATAAACAGGACTTCAAGACACATTTGGCTCAGAGA 1620
Db 1561 TGTGTGTGCGTGTATCTAGCCCTCATAAACAGGACTTCAAGACACATTTGGCTCAGAGA 1620
Qy 1621 CCCTAAGTCTCAAGGACAAAGCCACTAGTGAGAGAAATCTTTTGAAGGAGCTCAAACT 1680
Db 1621 CCCTAAGTCTCAAGGACAAAGCCACTAGTGAGAGAAATCTTTTGAAGGAGCTCAAACT 1680
Qy 1681 TTACAAGAAAGGATGTTTCTGAGATTTTGTATCTTACACCGCCATTTGGTGGGTGAG 1740
Db 1681 TTACAAGAAAGGATGTTTCTGAGATTTTGTATCTTACACCGCCATTTGGTGGGTGAG 1740
Qy 1741 GAACCACTGTGTTGTCTGTGAGCTTCTGTTTCTCGGAGGGAGGGTCAAGTGGG 1800
Db 1741 GAACCACTGTGTTGTCTGTGAGCTTCTGTTTCTCGGAGGGAGGGTCAAGTGGG 1800
Qy 1801 GAAAGGGGCAATTAAGATGTTTATTGGAACCTTTTCTGTTCTTCTGTTGTTTCTAA 1860
Db 1801 GAAAGGGGCAATTAAGATGTTTATTGGAACCTTTTCTGTTCTTCTGTTGTTTCTAA 1860
Qy 1861 AATTCACAGGAGAGCTTTTGGAGAGTCTCAAACTTAAGATGCTTTTAAAGAAAGGAG 1920
Db 1861 AATTCACAGGAGAGCTTTTGGAGAGTCTCAAACTTAAGATGCTTTTAAAGAAAGGAG 1920
Qy 1921 AAAAAAGTCTGTTATGCTGATTAAGTAAGTGTAGTGTGACTGAGAGACTCAGTACAGA 1980
Db 1921 AAAAAAGTCTGTTATGCTGATTAAGTAAGTGTAGTGTGACTGAGAGACTCAGTACAGA 1980
Qy 1981 CCTTTTAAATGCTGGTCATGTAATAATTTGCAAGTAGTAAGAAACGAAGGTGCAAGTG 2040
Db 1981 CCTTTTAAATGCTGGTCATGTAATAATTTGCAAGTAGTAAGAAACGAAGGTGCAAGTG 2040
Qy 2041 TACTGCTGGCAGGAGGTGATCATTAACCAAAAGTAACTTTGTTGGGTGGAGAGTTC 2100
Db 2041 TACTGCTGGCAGGAGGTGATCATTAACCAAAAGTAACTTTGTTGGGTGGAGAGTTC 2100
Qy 2101 TTTGTGAGAACTTGCATTTATTTGTCCTCCCTCATGTGTAGGTAGAAACATTTCTTAAT 2160
Db 2101 TTTGTGAGAACTTGCATTTATTTGTCCTCCCTCATGTGTAGGTAGAAACATTTCTTAAT 2160
Qy 2161 GCTGTGTACCTGCTCTGACATGTATGTTGGCATCTGTTATGCTAAAAGTTTTTCTGTA 2220
Db 2161 GCTGTGTACCTGCTCTGACATGTATGTTGGCATCTGTTATGCTAAAAGTTTTTCTGTA 2220
Qy 2221 CATGAACCTTGAAGACCTTACTACAAAACCTGTTGTTGGCCCCCATAGCAGGTGAA 2280
Db 2221 CATGAACCTTGAAGACCTTACTACAAAACCTGTTGTTGGCCCCCATAGCAGGTGAA 2280
Qy 2281 CTCAATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCAGTAAATATTTGCCCTTACGTAGT 2340
Db 2281 CTCAATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCAGTAAATATTTGCCCTTACGTAGT 2340
Qy 2341 TGTTTACCATTTTCAAGGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATT 2400
Db 2341 TGTTTACCATTTTCAAGGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATT 2400
Qy 2401 AATTTGCTTAATTTAGAGCTTCTATCCTCAAGCTTCTACCATTAACACAGCATATTA 2460
Db 2401 AATTTGCTTAATTTAGAGCTTCTATCCTCAAGCTTCTACCATTAACACAGCATATTA 2460

[illegible]

RESULT 2

RESOLUTION 2
US-09-542-615A-333
: Sequence 333. Application US/09542615A

; PALCILL NO. 6518236
: GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Kalos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy A.

APPLICANT: Fanger, Gary B.

APPLICANT: Fanger, Gary R.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
 TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C8

FILE REFERENCE: 11011143000
: CURRENT APPLICATION NUMBER: US/09/542.615A

CURRENT AFFILIATION NUMBER: 03/0
: CURRENT FILING DATE: 2000-04-14

;	CURRENT FILING DATE:	2000
:	NUMBER OF SEC ID NOS.	350

```

; NUMBER OF SEQ ID NOS: 350
: SOFTWARE: FastSeq for Windows Version 3.0

```

```

; SUFFIWARE: FASTSE
; CEO ID NO 333

```

```

; SEQ ID NO 333
.. LENGTH: 3916

```

LENGTH: 28
TYPE: DNA

TYPE: DNA
SPECANTCM: Homo sapiens

ORGANISM: HOMO

Query Match	100.0%;	Score 2816;	DB 4;	Length 2816;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2816;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TCGTTGTATCAAGACAGAGTGTGAAGGAAATCAATTTTCAAACTTTCACGGTGTGCCACCGT	60	
Db	1	TCGTTGTATCAAGACAGAGTGTGAAGGAAATCAATTTTCAAACTTTCACGGTGTGCCACCGT	60	
Qy	61	ACAGTACTGCCCTCACCCCTTACATCTCAGCGTTTCGTAGAAAACCCAGCTCATTTTCCTCTGG	120	
Db	61	ACAGTACTGCCCTCACCCCTTACATCTCAGCGTTTCGTAGAAAACCCAGCTCATTTTCCTCTGG	120	
Qy	121	AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGACAAATGAAATTCCTCAGT	180	
Db	121	AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGACAAATGAAATTCCTCAGT	180	
Qy	181	CCAGAGGTTTTCCAGCATATCTGGGATTTCTGGAACAGCCCTATATGTTTCAGTTTCAGCCC	240	
Db	181	CCAGAGGTTTTCCAGCATATCTGGGATTTCTGGAACAGCCCTATATGTTTCAGTTTCAGCCC	240	
Qy	241	ATTGACHTTGAACCTTTGTGGATGAAACCATCAGAAGATGGTGGCAAAACAAGATTGAGATT	300	
Db	241	ATTGACHTTGAACCTTTGTGGATGAAACCATCAGAAGATGGTGGCAAAACAAGATTGAGATT	300	

Qy	301	AGCATG	AGCTGTATCCGCATG	CAGGACTCGG	ACCTCGAGTGA	ACCCATGTG	GGCCACAGTAC	360		
Db	301	AGCATG	AGCTGTATCCGCATG	CAGGACTCGG	ACCTCGAGTGA	ACCCATGTG	GGCCACAGTAC	360		
Qy	361	ACGAAC	CTTGGGGCTCCTG	AACAGCATGG	AGCCAGCAGATT	CAGAAACGGCTCCT	CGTCCACC	420		
Db	361	ACGAAC	CTTGGGGCTCCTG	AACAGCATGG	AGCCAGCAGATT	CAGAAACGGCTCCT	CGTCCACC	420		
Qy	421	AGTCCCT	TATAACACAGAC	CAACGGCGAGAA	CAGCGTCA	CGCGGCCCTCGCCCT	TACGCACAG	480		
Db	421	AGTCCCT	TATAACACAGAC	CAACGGCGAGAA	CAGCGTCA	CGCGGCCCTCGCCCT	TACGCACAG	480		
Qy	481	CCGAGCT	CCACCTTCGATG	CTCTCTCCAT	CACCCGCCAT	CCCTCCAAAC	CCGACTAC	540		
Db	481	CCGAGCT	CCACCTTCGATG	CTCTCTCCAT	CACCCGCCAT	CCCTCCAAAC	CCGACTAC	540		
Qy	541	CGAGGCC	CGGACAGTTT	CGAAGTGTCTT	CCAGCAGT	CGAGCAAC	CGCGCAAGT	CGGCCACC	600	
Db	541	CGAGGCC	CGGACAGTTT	CGAAGTGTCTT	CCAGCAGT	CGAGCAAC	CGCGCAAGT	CGGCCACC	600	
Qy	601	TGGACCT	TATTCCACTG	CAACTGAAGAA	ACTCTACTG	CCAAATTC	CAAAAGACAT	CCCCCATC	660	
Db	601	TGGACCT	TATTCCACTG	CAACTGAAGAA	ACTCTACTG	CCAAATTC	CAAAAGACAT	CCCCCATC	660	
Qy	661	CAGATCA	AGGTGATGAT	ACCCCACTCT	CTCAGGGAGCT	GTATTCCG	CGCCATG	CGCTGTCTAC	720	
Db	661	CAGATCA	AGGTGATGAT	ACCCCACTCT	CTCAGGGAGCT	GTATTCCG	CGCCATG	CGCTGTCTAC	720	
Qy	721	AAAAAG	CTGAGCAGT	CAAGGAGTGT	GAAGCGTG	CGCCCAAC	ATGAGCTG	AGCGCGT	780	
Db	721	AAAAAG	CTGAGCAGT	CAAGGAGTGT	GAAGCGTG	CGCCCAAC	ATGAGCTG	AGCGCGT	780	
Qy	781	GAATTCA	ACAGGGACAG	ATTGCCCTCT	CTAGTCA	TTTGATTG	TCAGT	TAGAGGGGAACAGC	840	
Db	781	GAATTCA	ACAGGGACAG	ATTGCCCTCT	CTAGTCA	TTTGATTG	TCAGT	TAGAGGGGAACAGC	840	
Qy	841	CATGCC	CAGTATGTAGA	AGATCCCAT	CACAGGAAG	CAGAGTGT	GTGTTG	TACCTTATGAG	900	
Db	841	CATGCC	CAGTATGTAGA	AGATCCCAT	CACAGGAAG	CAGAGTGT	GTGTTG	TACCTTATGAG	900	
Qy	901	CAACCC	CAGGTGGCACT	GAAATTCAG	CAGCAGTCT	TGTACAA	TTTCA	TGTGTAA	CAGCAGT	960
Db	901	CAACCC	CAGGTGGCACT	GAAATTCAG	CAGCAGTCT	TGTACAA	TTTCA	TGTGTAA	CAGCAGT	960
Qy	961	TGTGTT	TGAGGGATGA	ACCGCGTCCAA	TTTTAA	TCATTTG	TACTCTG	GAAAC	CCAGAT	1020
Db	961	TGTGTT	TGAGGGATGA	ACCGCGTCCAA	TTTTAA	TCATTTG	TACTCTG	GAAAC	CCAGAT	1020
Qy	1021	GGGCA	AGTCTCTGGG	CGAGCTGCTTT	TGAGGCCGG	AGTCTGCT	TTGCC	CAGGAAGAC	1080	
Db	1021	GGGCA	AGTCTCTGGG	CGAGCTGCTTT	TGAGGCCGG	AGTCTGCT	TTGCC	CAGGAAGAC	1080	
Qy	1081	AGGAAG	CGCGATGA	AGATAGCAT	TCAGAA	AGCAGCAAGTTT	CGGACAGT	ACA	AGAACGGT	1140
Db	1081	AGGAAG	CGCGATGA	AGATAGCAT	TCAGAA	AGCAGCAAGTTT	CGGACAGT	ACA	AGAACGGT	1140
Qy	1141	GATGTT	ACCAAGCGG	CCGTTTCGT	CAGAA	CACATG	GTATCCAG	ATGAT	CCATCAAG	1200
Db	1141	GATGTT	ACCAAGCGG	CCGTTTCGT	CAGAA	CACATG	GTATCCAG	ATGAT	CCATCAAG	1200
Qy	1201	AAACGA	AGATCC	CCAGATG	AATCTGTT	TATATCTT	ACCA	GAGT	GGGGCCGT	1260
Db	1201	AAACGA	AGATCC	CCAGATG	AATCTGTT	TATATCTT	ACCA	GAGT	GGGGCCGT	1260
Qy	1261	GAAATG	CTGTTGA	AGATCA	AAAGTCC	CTTGGA	ACTCAT	GTAGT	ACTTCT	1320
Db	1261	GAAATG	CTGTTGA	AGATCA	AAAGTCC	CTTGGA	ACTCAT	GTAGT	ACTTCT	1320
Qy	1321	ATTGA	AACTGAC	AGGCAAC	AGCAG	CAGCAGC	ACCAT	CTTACT	TCAG	1380
Db	1321	ATTGA	AACTGAC	AGGCAAC	AGCAG	CAGCAGC	ACCAT	CTTACT	TCAG	1380

```
QY 1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAACAATCT 1440
Db 1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAACAATCT 1440
QY 1441 GACGCTCTTTTAGACATTCGAAGCCCGCAACCGATCAGTGTACCCATAGAGCCCTATC 1500
Db 1441 GACGCTCTTTTAGACATTCGAAGCCCGCAACCGATCAGTGTACCCATAGAGCCCTATC 1500
QY 1501 TCTATATTTTAAAGTGTGTGTGTATTTCCATGTGTATATGTAGTGTGTGTGTGTGT 1560
Db 1501 TCTATATTTTAAAGTGTGTGTGTATTTCCATGTGTATATGTAGTGTGTGTGTGTGT 1560
QY 1561 TGTGTGTGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620
Db 1561 TGTGTGTGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620
QY 1621 CCCAACTGCTCAAGGCAAAAGCCACCTAGTGTAGAGAACTTTTGAAGGGACTCAAACT 1680
Db 1621 CCCAACTGCTCAAGGCAAAAGCCACCTAGTGTAGAGAACTTTTGAAGGGACTCAAACT 1680
QY 1681 TTACAAGAAAGATGTTTTCTGCAGATTTTGTATCCTTAGACCGGCCATTGCTGGTGAG 1740
Db 1681 TTACAAGAAAGATGTTTTCTGCAGATTTTGTATCCTTAGACCGGCCATTGCTGGTGAG 1740
QY 1741 GAAACACTGTGTTTCTGTGAGCTTTCTGTGTTTCTCTGGAGGGGCTCAGGTGG 1800
Db 1741 GAAACACTGTGTTTCTGTGAGCTTTCTGTGTTTCTCTGGAGGGGCTCAGGTGG 1800
QY 1801 GAAAGGGCAATAGATGTTTATTTGGAACCCCTTTCTCTCTCTCTCTCTCTCTCTCTAA 1860
Db 1801 GAAAGGGCAATAGATGTTTATTTGGAACCCCTTTCTCTCTCTCTCTCTCTCTCTCTAA 1860
QY 1861 AATTCACAGGGAAGCTTTTGAGCAGGCTCTCAAACTTAAGATGCTCTTTTAAAGAAAGAG 1920
Db 1861 AATTCACAGGGAAGCTTTTGAGCAGGCTCTCAAACTTAAGATGCTCTTTTAAAGAAAGAG 1920
QY 1921 AAAAAGTTGTTATTTCTGTGCTAATAGTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1980
Db 1921 AAAAAGTTGTTATTTCTGTGCTAATAGTTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1980
QY 1981 CCCTTTTAACTGCTGCTAATTAATTAATTTGCAAGTAGTAAAGAAAGGAGTGTCAAGTG 2040
Db 1981 CCCTTTTAACTGCTGCTAATTAATTAATTTGCAAGTAGTAAAGAAAGGAGTGTCAAGTG 2040
QY 2041 TACTGCTGGCAGCAGGAGTGTATCAATCAAAAGTAATCAACTTTGTGGTGGAGAGTTC 2100
Db 2041 TACTGCTGGCAGCAGGAGTGTATCAATCAAAAGTAATCAACTTTGTGGTGGAGAGTTC 2100
QY 2101 TTTGTGAAACTTGCATTTATTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTAAT 2160
Db 2101 TTTGTGAAACTTGCATTTATTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTTAAT 2160
QY 2161 GCTGTGACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Db 2161 GCTGTGACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
QY 2221 CATGAAACCTTGAAGACCTACTACAAAACCTGTTGTTGGCCCCCATAGCAGGTGAA 2280
Db 2221 CATGAAACCTTGAAGACCTACTACAAAACCTGTTGTTGGCCCCCATAGCAGGTGAA 2280
QY 2281 CTCATTTTGTGCTTTTATAGAAAGCAAAATCCACCCAGTAATTAATTCCTCTTACGTAGT 2340
Db 2281 CTCATTTTGTGCTTTTATAGAAAGCAAAATCCACCCAGTAATTAATTCCTCTTACGTAGT 2340
QY 2341 TGTTTACCATTTATCAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTGTGATT 2400
Db 2341 TGTTTACCATTTATCAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTGTGATT 2400
QY 2401 AATTTGCTTAATAGAGCTTCTATCCCTCAAGCCTACCTACCATTAACCCAGCCATATTA 2460
Db 2401 AATTTGCTTAATAGAGCTTCTATCCCTCAAGCCTACCTACCATTAACCCAGCCATATTA 2460
QY 2461 CTGATACCTGTTCAAGTGTATTTAGCCAGGAGACTTACGTTTGTAGTGAAGTCCCAAGC 2520
```

```
Db 2461 CTGATACCTGTTCAAGTGTATTTAGCCAGGAGACTTACGTTTGTAGTGAAGTCCCAAGC 2520
QY 2521 AGAGCTGTTAAATCAGACACTCTCGGACTGGAAATTAAGATTTGAAGGGTAGACTACTT 2580
Db 2521 AGAGCTGTTAAATCAGACACTCTCGGACTGGAAATTAAGATTTGAAGGGTAGACTACTT 2580
QY 2581 TTTCTTTTTTACTCAAAAGTTTAGAGAACTCTCTGTTTCTTTTCCATTTTAAAAACATATT 2640
Db 2581 TTTCTTTTTTACTCAAAAGTTTAGAGAACTCTCTGTTTCTTTTCCATTTTAAAAACATATT 2640
QY 2641 TTAAGATAATAGCATAAAGACTTTTAAAAATGTTTCTCCCTCCATCTTCCACACCCAGT 2700
Db 2641 TTAAGATAATAGCATAAAGACTTTTAAAAATGTTTCTCCCTCCATCTTCCACACCCAGT 2700
QY 2701 CACCAGCACTGTATTTTCTGTCCCAAGACAAATGATTTCTGTTATTGAGGCTGTGCTT 2760
Db 2701 CACCAGCACTGTATTTTCTGTCCCAAGACAAATGATTTCTGTTATTGAGGCTGTGCTT 2760
QY 2761 TTTGGGATGTGTGATTTTAAATTTTCAATAAACCTTTGCACTTTGTTTAAAGAAA 2816
Db 2761 TTTGGGATGTGTGATTTTAAATTTTCAATAAACCTTTGCACTTTGTTTAAAGAAA 2816
```

RESULT 3

US-09-606-421B-333
; Sequence 333 Application US/09506421B
; Patent No. 531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-333

methad w/ 250

Query Match 100.0%; Score 2816; DB 4; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTTGATATCAAGACAGTTGAAGAAATGAATTTTGAACCTTCAAGGTGTGCCACCT 60
Db 1 TCGTTGATATCAAGACAGTTGAAGAAATGAATTTTGAACCTTCAAGGTGTGCCACCT 60
QY 61 ACAGTACTGCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTTTGG 120
Db 61 ACAGTACTGCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTTTGG 120
QY 121 AAAGAAAGTTATTTACCATCCACCATGTCACAGACACAGACAAATGAATTTCTCAGT 180
Db 121 AAAGAAAGTTATTTACCATCCACCATGTCACAGACACAGACAAATGAATTTCTCAGT 180
QY 181 CCAGAGTTTCCAGCATATCTGGCAATTTCTGAAACAGCCCTATATGTTAGTTCAGGCC 240
Db 181 CCAGAGTTTCCAGCATATCTGGCAATTTCTGAAACAGCCCTATATGTTAGTTCAGGCC 240
QY 241 ATTGACTTGAACCTTTGTGGATGAACCATCAAGAGATGGTGGCAGAAACAAGATTGAGATT 300
Db 241 ATTGACTTGAACCTTTGTGGATGAACCATCAAGAGATGGTGGCAGAAACAAGATTGAGATT 300

241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGGTGGACAAAACAAGATTGAGATT 300
301 AGCATGGACTGTATCCGATCGAGACTCGGACCTCGAGTGAGTGAACCCATGTGGCCACAGTAC 360
301 AGCATGGACTGTATCCGATCGAGACTCGGACCTCGAGTGAGTGAACCCATGTGGCCACAGTAC 360
361 AGCAACCTGGGGCTCTGTAAACAGCATGGAACGAGAGATTCAGAACGGCTCTCTGTCACCC 420
361 AGCAACCTGGGGCTCTGTAAACAGCATGGAACGAGAGATTCAGAACGGCTCTCTGTCACCC 420
421 AGTCCTTATAACACAGACACCGCGCAGACAGGTTCACGGCCCTCGCCCTACGACAG 480
421 AGTCCTTATAACACAGACACCGCGCAGACAGGTTCACGGCCCTCGCCCTACGACAG 480
481 CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCGCCATCCCTCCAAACCGACTAC 540
481 CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCGCCATCCCTCCAAACCGACTAC 540
541 CCAGCCCGCACAGTTTCGACGTGCTCTTCCAGCAGTGGAGCACCGCCCAAGTCGGCCACC 600
541 CCAGCCCGCACAGTTTCGACGTGCTCTTCCAGCAGTGGAGCACCGCCCAAGTCGGCCACC 600
601 TGGAGTATTCACCTGAACCTGAAGAACTCTACTGCCAAATTCGAAAGACATGCCCCATC 660
601 TGGAGTATTCACCTGAACCTGAAGAACTCTACTGCCAAATTCGAAAGACATGCCCCATC 660
661 CAGATCAAGGTGATGACCCCACTCTCTCAGGGAGCTGTTATCCGGCCATGCTGCTAC 720
661 CAGATCAAGGTGATGACCCCACTCTCTCAGGGAGCTGTTATCCGGCCATGCTGCTAC 720
721 AAAAAGCTGACACGTCAACGAGGTGGTGAAGCGTGCGCCCAACCATGAGTGAAGCCGT 780
721 AAAAAGCTGACACGTCAACGAGGTGGTGAAGCGTGCGCCCAACCATGAGTGAAGCCGT 780
781 GAAATCAAGAGGGACAGATTGCCCTCTAGTCAATTTGATTCGAGTAGAGGGAAACAGC 840
781 GAAATCAAGAGGGACAGATTGCCCTCTAGTCAATTTGATTCGAGTAGAGGGAAACAGC 840
841 CATGCCAGTATGTAGAAGATCCCATCACGAAGACAGAGTGTCTGTACTTTATGAG 900
841 CATGCCAGTATGTAGAAGATCCCATCACGAAGACAGAGTGTCTGTACTTTATGAG 900
901 CCACCCAGGTGGCACTGAATTCAGACAGTCTTTGTACAAATTCATGTGTAAACAGCAGT 960
901 CCACCCAGGTGGCACTGAATTCAGACAGTCTTTGTACAAATTCATGTGTAAACAGCAGT 960
961 TGTGTGAGGAGTGAACCGCCGTCCAATTTAAATCAATTTGTTACTCTGGAACACAGAGAT 1020
961 TGTGTGAGGAGTGAACCGCCGTCCAATTTAAATCAATTTGTTACTCTGGAACACAGAGAT 1020
1021 GGGCAAGTCTGGGCCGAGCTGCTTTGAGGCCCGGATCTGTGCTTTGCCAGGAAGAGAC 1080
1021 GGGCAAGTCTGGGCCGAGCTGCTTTGAGGCCCGGATCTGTGCTTTGCCAGGAAGAGAC 1080
1081 AGGAAGCGGATGAAGATAGCATCAGAAGCAGCAAGTTTCGACAGTACAAAGAACGGT 1140
1081 AGGAAGCGGATGAAGATAGCATCAGAAGCAGCAAGTTTCGACAGTACAAAGAACGGT 1140
1141 GATGTAGACAGCGCCGCTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
1141 GATGTAGACAGCGCCGCTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
1201 AAACGAAGTCCCAGATGATGAACCTGTTTACTTACCAGTGAGGGCGGTGAGACTTAT 1260
1201 AAACGAAGTCCCAGATGATGAACCTGTTTACTTACCAGTGAGGGCGGTGAGACTTAT 1260
1261 GAAATGCTGTGAAGATCAAGAGTCCCTGGAACTCATGCACTCATGCACTCATGCACTCAT 1320
1261 GAAATGCTGTGAAGATCAAGAGTCCCTGGAACTCATGCACTCATGCACTCATGCACTCAT 1320
1321 ATTGAAACGTACAGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
1321 ATTGAAACGTACAGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380

1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAAACTCCAAAAAATCT 1440
1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAAACTCCAAAAAATCT 1440
1441 GACGCTCTCTTTAGACATTCCAAGCCCAACCGATCAGTGTACCCATAGAGCCCTATC 1500
1441 GACGCTCTCTTTAGACATTCCAAGCCCAACCGATCAGTGTACCCATAGAGCCCTATC 1500
1501 TCTATATTTTAAAGTGTGTGTATTTTCATGTGTATATCTGAGTGTGTGTGTGTA 1560
1501 TCTATATTTTAAAGTGTGTGTATTTTCATGTGTATATCTGAGTGTGTGTGTGTA 1560
1561 TGTGTGCGTGTGTATCTAGCCCTCATATAACAGGACTTTGAAGACACATTTGGCTCAGAGA 1620
1561 TGTGTGCGTGTGTATCTAGCCCTCATATAACAGGACTTTGAAGACACATTTGGCTCAGAGA 1620
1621 CCCAACTGCTCAAAAGGCACAAAGCCACTAGTGAGAGAAATCTTTTGAAGGACTCAAACT 1680
1621 CCCAACTGCTCAAAAGGCACAAAGCCACTAGTGAGAGAAATCTTTTGAAGGACTCAAACT 1680
1681 TTACAAGAAAGGATGTTTTCTGCAGATTTTCTATCTTAGCCGCAATTTGGTGGGTGAG 1740
1681 TTACAAGAAAGGATGTTTTCTGCAGATTTTCTATCTTAGCCGCAATTTGGTGGGTGAG 1740
1741 GAAACCACTGCTTCTGTGAGCTTTCTGTTGTTTCTGGGAGGAGGGGTGAGTGGG 1800
1741 GAAACCACTGCTTCTGTGAGCTTTCTGTTGTTTCTGGGAGGAGGGGTGAGTGGG 1800
1801 GAAAGGGCAATAAGATGTTTTATTGGAAACCTTTCTGCTCTCTCTGTTGTTTTCTAA 1860
1801 GAAAGGGCAATAAGATGTTTTATTGGAAACCTTTCTGCTCTCTCTGTTGTTTTCTAA 1860
1861 AATTACAGGAGGAGCTTTTGAGCAGGTCTCAAACTTAAAGATGCTTTTAAAGAAAGGAG 1920
1861 AATTACAGGAGGAGCTTTTGAGCAGGTCTCAAACTTAAAGATGCTTTTAAAGAAAGGAG 1920
1921 AAAAAGGTGTTATTGCTGTGCATTAAGTAAGTTGTAGTGACTCAGAGACTCAGTCAGA 1980
1921 AAAAAGGTGTTATTGCTGTGCATTAAGTAAGTTGTAGTGACTCAGAGACTCAGTCAGA 1980
1981 CCTTTTAACTGCTGGTCATGTAATAATTGCAAGTAGTAAGAAACGAGAGGTGTCAAGTG 2040
1981 CCTTTTAACTGCTGGTCATGTAATAATTGCAAGTAGTAAGAAACGAGAGGTGTCAAGTG 2040
2041 TACTGCTGGCAGCGAGTGATCATTAACAAAGTAATCAACTTTTGGTGGTGGAGGTTTC 2100
2041 TACTGCTGGCAGCGAGTGATCATTAACAAAGTAATCAACTTTTGGTGGTGGAGGTTTC 2100
2101 TTTGTGAGAACTTGCATTTATTGTCCTCCCTCATGTGTAGGTAGAACATTTCTTAAT 2160
2101 TTTGTGAGAACTTGCATTTATTGTCCTCCCTCATGTGTAGGTAGAACATTTCTTAAT 2160
2161 GCTGTGACCTGCTGCGCACTGTATGTTGGCATCTGTTATGCTTAAAGTTTTCTTGTGA 2220
2161 GCTGTGACCTGCTGCGCACTGTATGTTGGCATCTGTTATGCTTAAAGTTTTCTTGTGA 2220
2221 CATGAAACCTGGAGAGCTACTACAAAACCTGTTGTTGGCCCCCATAGCAGTGAA 2280
2221 CATGAAACCTGGAGAGCTACTACAAAACCTGTTGTTGGCCCCCATAGCAGTGAA 2280
2281 CTCAATTTTGTCTTTTAAATAGAAAGACAAATCCACCCAGTAATAATTGCCCTTAGCTAGT 2340
2281 CTCAATTTTGTCTTTTAAATAGAAAGACAAATCCACCCAGTAATAATTGCCCTTAGCTAGT 2340
2341 TGTTTACATTAATCAAGCTCAAAAATAGAAATTTGAAGCCCTCTCAGAAAAATCTGTGAT 2400
2341 TGTTTACATTAATCAAGCTCAAAAATAGAAATTTGAAGCCCTCTCAGAAAAATCTGTGAT 2400
2401 AATTGCTTAATAGAGCTTCTATCCCTCAAGCCCTACCTACCATAAAAACAGCCATATTA 2460
2401 AATTGCTTAATAGAGCTTCTATCCCTCAAGCCCTACCTACCATAAAAACAGCCATATTA 2460

Qy 2461 CTGATCTGTTTCAGTGCACTTTAGCCAGGAGACTTACGTTTTGAGTAAGTGAAGTCCCAAGC 2520
Db |||||
2461 CTGATCTGTTTCAGTGCACTTTAGCCAGGAGACTTACGTTTTGAGTAAGTGAAGTCCCAAGC 2520
Qy 2521 AGACGTGTTAAATCAGCACTCTCGGACTGGAACTTAAAGATTGAAGGGTAGACTACTT 2580
Db |||||
2521 AGACGTGTTAAATCAGCACTCTCGGACTGGAACTTAAAGATTGAAGGGTAGACTACTT 2580
Qy 2581 TTTCTTTTTTACTCAAAAGTTTGAAGAACTCTGTTTTCTTTTCCATTTTAAACACATATT 2640
Db |||||
2581 TTTCTTTTTTACTCAAAAGTTTGAAGAACTCTGTTTTCTTTTCCATTTTAAACACATATT 2640
Qy 2641 TTAAGATAATAGCATAAAGACTTTAAATAAGTTTCTCCCTCCATCTTCCACACCCAGT 2700
Db |||||
2641 TTAAGATAATAGCATAAAGACTTTAAATAAGTTTCTCCCTCCATCTTCCACACCCAGT 2700
Qy 2701 CACGAGCACTGATTTTCTGTCACCAAGCAATGATTTCTTTGTTATTGAGGCTGTGCTT 2760
Db |||||
2701 CACGAGCACTGATTTTCTGTCACCAAGCAATGATTTCTTTGTTATTGAGGCTGTGCTT 2760
Qy 2761 TTGTGGATGTCGTGATTTTAAATTTTCAATAAACTTTTGCATCTTGGTTTAAAGAAA 2816
Db |||||
2761 TTGTGGATGTCGTGATTTTAAATTTTCAATAAACTTTTGCATCTTGGTTTAAAGAAA 2816

RESULT 4

US-09-630-940B-333
; Sequence 333, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-333

Query Match 100.0%; Score 2816; DB 4; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCGTTGATATCAAGACAGAGTTGAAGGAAATGAATTTTGAACCTTCAACGGTGTGCCACCT 60
Db |||||
1 TCGTTGATATCAAGACAGAGTTGAAGGAAATGAATTTTGAACCTTCAACGGTGTGCCACCT 60
Qy 61 ACAGTACTGCGCTGACCCCTTACATCCAGCGTTTGTAGAAACCCAGCTCAATTTCTCTGG 120
Db |||||
61 ACAGTACTGCGCTGACCCCTTACATCCAGCGTTTGTAGAAACCCAGCTCAATTTCTCTGG 120
Qy 121 AAGAAAGTTATTACCGATCCACATGTCACAGACACACAGACAAATGAATTTCTCTAGT 180
Db |||||
121 AAGAAAGTTATTACCGATCCACATGTCACAGACACACAGACAAATGAATTTCTCTAGT 180
Qy 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTTATATGTTTCAGTTTCAGCCC 240
Db |||||
181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTTATATGTTTCAGTTTCAGCCC 240

Qy 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAGATGGTGGCAACAAACAGATTGAGATT 300
Db |||||
241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAGATGGTGGCAACAAACAGATTGAGATT 300
Qy 301 AGCATGAGCTGTATTCGCACTGCAAGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC 360
Db |||||
301 AGCATGAGCTGTATTCGCACTGCAAGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC 360
Qy 361 ACAGACCTGGGGTCTCTGAACAGCATGACAGATTCAGAAACAGGCTCTCTGTCACAC 420
Db |||||
361 ACAGACCTGGGGTCTCTGAACAGCATGACAGATTCAGAAACAGGCTCTCTGTCACAC 420
Qy 421 AGTCCCTTATAACACAGACACCGCGCAGACAGGCTCACGGCGCCTCGCCCTACGCACAG 480
Db |||||
421 AGTCCCTTATAACACAGACACCGCGCAGACAGGCTCACGGCGCCTCGCCCTACGCACAG 480
Qy 481 CCAGCTCCACCTTCGATGCTCTCTCCATCACCCTCCATCCCTCCACACCGACTAC 540
Db |||||
481 CCAGCTCCACCTTCGATGCTCTCTCCATCACCCTCCATCCCTCCACACCGACTAC 540
Qy 541 CCAGGCGCGCACAGTTTCGACGCTGCTTCCAGCAGTCGAGCACCGCAAGTCGGCCACC 600
Db |||||
541 CCAGGCGCGCACAGTTTCGACGCTGCTTCCAGCAGTCGAGCACCGCAAGTCGGCCACC 600
Qy 601 TGGACGTATTCCACTGAACCTGAAGAACTCTCTACTGCCAAATTTGCAAGACATGCCCCATC 660
Db |||||
601 TGGACGTATTCCACTGAACCTGAAGAACTCTCTACTGCCAAATTTGCAAGACATGCCCCATC 660
Qy 661 CAGATCAAGGTGATGACCCCACTCTCAGGAGCTGTTATCCGCGCATGCCCTGTCTAC 720
Db |||||
661 CAGATCAAGGTGATGACCCCACTCTCAGGAGCTGTTATCCGCGCATGCCCTGTCTAC 720
Qy 721 AAAAAAGCTCAGCACGTCACGGAGGTGTGAAGGGTGTGCGGAGTGTGCTGAGCCGT 780
Db |||||
721 AAAAAAGCTCAGCACGTCACGGAGGTGTGAAGGGTGTGCGGAGTGTGCTGAGCCGT 780
Qy 781 GAATTTCAACGAGGACAGATTGGCCCTCTAGTCAATTTGATTTCCAGTAGAGGGAACAGC 840
Db |||||
781 GAATTTCAACGAGGACAGATTGGCCCTCTAGTCAATTTGATTTCCAGTAGAGGGAACAGC 840
Qy 841 CATGCCAGTATGTAGAAGATCCCATCAGAGGAAGACAGAGTGTGCTGTTACCTTATGAG 900
Db |||||
841 CATGCCAGTATGTAGAAGATCCCATCAGAGGAAGACAGAGTGTGCTGTTACCTTATGAG 900
Qy 901 CCACCCAGGTTGCGACTGAATTCACGACAGTCTTGTACAAATTTTCAATTTTCAATTTT 960
Db |||||
901 CCACCCAGGTTGCGACTGAATTCACGACAGTCTTGTACAAATTTTCAATTTTCAATTTT 960
Qy 961 TGTGTTGGAGGGATGAACCCCGTCCAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1020
Db |||||
961 TGTGTTGGAGGGATGAACCCCGTCCAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 1020
Qy 1021 GGGCAAGTCTCGGCCCGACGCTGCTTTGAGCCCGGATCTGTGCTTGGCCAGGAGAGAC 1080
Db |||||
1021 GGGCAAGTCTCGGCCCGACGCTGCTTTGAGCCCGGATCTGTGCTTGGCCAGGAGAGAC 1080
Qy 1081 AGGAAGCGGATGAAGTAGCATCAGAAAGCAGCAAGTTTCGGAAGTGTACAAAGAACCGT 1140
Db |||||
1081 AGGAAGCGGATGAAGTAGCATCAGAAAGCAGCAAGTTTCGGAAGTGTACAAAGAACCGT 1140
Qy 1141 GATGGTACGAAGCGCCGCTTTCGTGAGAACACATCGGTATCCAGATGACATCCATCAAG 1200
Db |||||
1141 GATGGTACGAAGCGCCGCTTTCGTGAGAACACATCGGTATCCAGATGACATCCATCAAG 1200
Qy 1201 AAACGAAGATCCCGAGATGATGAATCTGTTATCTTACAGTGAAGGGCCGTGAGCTTAT 1260
Db |||||
1201 AAACGAAGATCCCGAGATGATGAATCTGTTATCTTACAGTGAAGGGCCGTGAGCTTAT 1260
Qy 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGAACTCATGAGTACCTTCTCCTCAGCACACA 1320
Db |||||
1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGAACTCATGAGTACCTTCTCCTCAGCACACA 1320

Qy 240 CATTGACTTGAACCTTTGTGGATGAACCATCAGAAAGTGGTCGCAACCAAGATTGAGAT 299
Db 241 CATTGACTTGAACCTTTGTGGATGAACCATCAGAAAGTGGTCGCAACCAAGATTGAGAT 300
Qy 300 TAGCATGACCTGTATCCGCATCGAGGACTCGGAAGCTGAGTGACCCCATGTGGCCACAGTA 359
Db 301 TAGCATGACCTGTATCCGCATCGAGGACTCGGAAGCTGAGTGACCCCATGTGGCCACAGTA 360
Qy 360 CACGAACCTGGGGCTCCTGAACAGCATGGACCGACAGATTCCAGAACCGCTCCTCGTCCAC 419
Db 361 CACGAACCTGGGGCTCCTGAACAGCATGGACCGACAGATTCCAGAACCGCTCCTCGTCCAC 420
Qy 420 CAGTCCCTATAACACAGACCAACCGCAGAAACAGCGTCAACCGCCCTCGCCCTACGCACA 479
Db 421 CAGTCCCTATAACACAGACCAACCGCAGAAACAGCGTCAACCGCCCTCGCCCTACGCACA 480
Qy 480 GCCAGCTCCACCTTCGATGCTCTCTCCATCAGCGTCAACCGCCCTCCACACCGACTA 539
Db 481 GCCAGCTCCACCTTCGATGCTCTCTCCATCAGCGTCAACCGCCCTCCACACCGACTA 540
Qy 540 CCCAGGCCGCACAGTTTTCGACGCTCTCTCCAGCGTTCGAGCACCGCCCAAGTCGGCCAC 599
Db 541 CCCAGGCCGCACAGTTTTCGACGCTCTCTCCAGCGTTCGAGCACCGCCCAAGTCGGCCAC 600
Qy 600 CTGACGCTATTCCACTGAACTGAAGAACTCTACTGCCAAATTGCAAGACATGCCCCAT 659
Db 601 CTGACGCTATTCCACTGAACTGAAGAACTCTACTGCCAAATTGCAAGACATGCCCCAT 660
Qy 660 CCAGATCAAGGTGATGACCCACCTCTCTCAGGAGCTGTATTCGCGGCCATGCTGTCTA 719
Db 661 CCAGATCAAGGTGATGACCCACCTCTCTCAGGAGCTGTATTCGCGGCCATGCTGTCTA 720
Qy 720 CAATAAAGCTGAGCACGTCACGAGGTGGTGAAGCGTCCCAACCATGAGCTGAGCCG 779
Db 721 CAATAAAGCTGAGCACGTCACGAGGTGGTGAAGCGTCCCAACCATGAGCTGAGCCG 780
Qy 780 TGAATTCAACAGGAGCAGATTGCCCCCTCTAGTCAATTGATTCGAGTAGAGGGAAACAG 839
Db 781 TGAATTCAACAGGAGCAGATTGCCCCCTCTAGTCAATTGATTCGAGTAGAGGGAAACAG 840
Qy 840 CCATGCCAGCTATGTAGAGATCCATCAGAGGAGCAGAGTGTCTGTACCTTATGA 899
Db 841 CCATGCCAGCTATGTAGAGATCCATCAGAGGAGCAGAGTGTCTGTACCTTATGA 900
Qy 900 GCCACCCAGGTTGGCACTGAAATTCACGACAGTCTTGACAAATTCATGTGTAAACAGCAG 959
Db 901 GCCACCCAGGTTGGCACTGAAATTCACGACAGTCTTGACAAATTCATGTGTAAACAGCAG 960
Qy 960 TTGTGTTGGAGGATGAACCGCCCTCCAAATTTTAAATCAATGTTACTCTGGAAACAGAGA 1019
Db 961 TTGTGTTGGAGGATGAACCGCCCTCCAAATTTTAAATCAATGTTACTCTGGAAACAGAGA 1020
Qy 1020 TGGGCAAGTCTGGGCGAGCCTGTTGAGGCCGGATCTGTCTGTGGCCAGGAGAGA 1079
Db 1021 TGGGCAAGTCTGGGCGAGCCTGTTGAGGCCGGATCTGTCTGTGGCCAGGAGAGA 1080
Qy 1080 CAGGAAGCGCATGAAGATAGCATCAGAAACAGCAAGTTTCGACAGTACAAAGAACGG 1139
Db 1081 CAGGAAGCGCATGAAGATAGCATCAGAAACAGCAAGTTTCGACAGTACAAAGAACGG 1140
Qy 1140 TGATGGTACGAAGCGCCGTTTCGTCAGAACACATGGTATCCAGATGACATCCATCAA 1199
Db 1141 TGATGGTACGAAGCGCCGTTTCGTCAGAACACATGGTATCCAGATGACATCCATCAA 1200
Qy 1200 GAAACGAAGATCCCGAGATGAACTGTTATATTACAGTGAGGGCCGTGAGACTTA 1259
Db 1201 GAAACGAAGATCCCGAGATGAACTGTTATATTACAGTGAGGGCCGTGAGACTTA 1260
Qy 1260 TGAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGACAGTCTCTCTCAGCACAC 1319
Db 1261 TGAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGACAGTCTCTCTCAGCACAC 1320
Qy 1320 AATTGAAACGTACAGGCAACGCAACAGCAGCAGCACCAGCACTTACTTCAGAAACATCT 1379

Db 1321 AATTGAAACGTACAGGCAACAGCAACAGCAGCAGCACCAGCACTTACTTCAGAAACATCT 1380
Qy 1380 CTTTTCAGCCTGCTTCAGGAATCAGCTTGTGGAGCCCGGAGAGAAACTCCAAACCAATC 1439
Db 1381 CTTTTCAGCCTGCTTCAGGAATCAGCTTGTGGAGCCCGGAGAGAAACTCCAAACCAATC 1440
Qy 1440 TGACGCTCTTCTTTAGACATTTCCAAAGCCCCCAACCGATCAGTGTACCATAGAGCCCTAT 1499
Db 1441 TGACGCTCTTCTTTAGACATTTCCAAAGCCCCCAACCGATCAGTGTACCATAGAGCCCTAT 1500
Qy 1500 CTCTATATTTTAAGTGTGTGTGTATTTCCATGTGTATATGTGAGTGTGTGTGTGT 1559
Db 1501 CTCTATATTTTAAGTGTGTGTGTATTTCCATGTGTATATGTGAGTGTGTGTGTGT 1560
Qy 1560 ATGTGTGTGTGTGTGTATCTAGCCCTCATAAAACAGGACTTTGAAGACACTTTGGCTCAGAG 1619
Db 1561 ATGTGTGTGTGTGTATCTAGCCCTCATAAAACAGGACTTTGAAGACACTTTGGCTCAGAG 1620
Qy 1620 ACCCAACTGCTCAAGAGCACAAGCCACTAGTGTAGAGAAATCTTTGAAGGACTCAAAACC 1679
Db 1621 ACCCAACTGCTCAAGAGCACAAGCCACTAGTGTAGAGAAATCTTTGAAGGACTCAAAACC 1680
Qy 1680 TTACAGAAAGGATGTTTCTGCAGATTTTGTATCTCTTAGACCGGCCATTTGGTGGGTGA 1739
Db 1681 TTACAGAAAGGATGTTTCTGCAGATTTTGTATCTCTTAGACCGGCCATTTGGTGGGTGA 1740
Qy 1740 GGAACCACTGT 1799
Db 1741 GGAACCACTGT 1800
Qy 1800 GGAAGGGGCAATTAAGATGTTTATGGAACCCCTTTCTGTCTCTCTGTGTGTGTGTGT 1859
Db 1801 GGAAGGGGCAATTAAGATGTTTATGGAACCCCTTTCTGTCTCTCTGTGTGTGTGTGT 1860
Qy 1860 AAATTCACAGGGAAGCTTTTGACAGGCTCTCAAACTTAAGATGCTTTTAAAGAAAGGA 1919
Db 1861 AAATTCACAGGGAAGCTTTTGACAGGCTCTCAAACTTAAGATGCTTTTAAAGAAAGGA 1920
Qy 1920 GAAAAAGTTGTTATTTGCTGTGTGCTGCAATAAGTTAGTGTAGGTGACTGAGAGACTCAGTCAG 1979
Db 1921 GAAAAAGTTGTTATTTGCTGTGTGCTGCAATAAGTTAGTGTAGGTGACTGAGAGACTCAGTCAG 1980
Qy 1980 ACCCTTTTAATGCTGTGCTGATTAATAATATGCAAGTAGTAAAGAACGAGGTGTCAAGT 2039
Db 1981 ACCCTTTTAATGCTGTGCTGATTAATAATATGCAAGTAGTAAAGAACGAGGTGTCAAGT 2040
Qy 2040 GTACTGCTGGCAGCGAGGTGATCATACCAAAAGTAATCAACTTTCTGTGGTGGAGAGTT 2099
Db 2041 GTACTGCTGGCAGCGAGGTGATCATACCAAAAGTAATCAACTTTCTGTGGTGGAGAGTT 2100
Qy 2100 CTTTGTGAGAACTTGGCAATTTTGTGTCTCTCCCTCATGTGTAGTGTAGTGTAGTGTAGT 2159
Db 2101 CTTTGTGAGAACTTGGCAATTTTGTGTCTCTCCCTCATGTGTAGTGTAGTGTAGTGTAGT 2160
Qy 2160 TGCTGTGTACTGCTGCTGCCACTGTATGTGTGGCATCTGTATGCTAAAGTGTGTGTGTGT 2219
Db 2161 TGCTGTGTACTGCTGCTGCCACTGTATGTGTGGCATCTGTATGCTAAAGTGTGTGTGTGT 2220
Qy 2220 ACATGAACCTTGGAGACCTTACTACAAAAAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2279
Db 2221 ACATGAACCTTGGAGACCTTACTACAAAAAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2280
Qy 2280 ACTCATTTTGTGTCTTTTAAATAGAAAGCAAAATCCACCCCAAGTAAATTTGCCCTTACGTTAG 2339
Db 2281 ACTCATTTTGTGTCTTTTAAATAGAAAGCAAAATCCACCCCAAGTAAATTTGCCCTTACGTTAG 2340
Qy 2340 TTGTTTACCAATTAATCAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAATCTGTGAT 2399
Db 2341 TTGTTTACCAATTAATCAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAATCTGTGAT 2400
Qy 2400 TAATTTGCTTAATTAGAGCTTCTATCCCTCAGGCTTACCTACCATTAACACAGCCATATT 2459

Db 253506 TATTTTAAGATAATAGCAATAAGAACTTTAAATAATGTTCTCCCTCCCTCATCTTCCACACC 253565
Qy 2697 CAGTCACAGCACTGATTTTCTGTCACCAAGACAATGATTTCTTTGTTATTGAGCGCTGTT 2756
Db 253566 CAGTCACAGCACTGATTTTCTGTCACCAAGACAATGATTTCTTTGTTATTGAGCGCTGTT 253625
Qy 2757 GCTTTTGTGGATGTGTGATTTTAAATTTTCAATFAAACTTTTGCATCTTGGTTTA 2809
Db 253626 GCTTTTGTGGATGTGTGATTTTAAATTTTCAATFAAACTTTTGCATCTTGGTTTA 253678

RESULT 7

US-09-643-597-332

; Sequence 332, Application US/09643597

; Patent No. 6426072

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643.597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 332

; LENGTH: 2270

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-643-597-332

Query Match 48.9%; Score 1376; DB 3; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTTGATATCAAGACAGAGTTGAAGCAATGAAATTTGAAACTTCCAGCGTGTGCCACCT 60
Db 1 TCGTTGATATCAAGACAGAGTTGAAGCAATGAAATTTGAAACTTCCAGCGTGTGCCACCT 60

Qy 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTTTGG 120
Db 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTTTGG 120

Qy 121 AAAGAAAGTTATACCGATCCACCATGTCCAGACACACAGACAATGAATTCCTCAGT 180
Db 121 AAAGAAAGTTATACCGATCCACCATGTCCAGACACACAGACAATGAATTCCTCAGT 180

Qy 181 CCAGAGGTTTCCAGCATATCGGATTTTCTGGAACAGCTATATGTTTCAGTTCCAGCCC 240
Db 181 CCAGAGGTTTCCAGCATATCGGATTTTCTGGAACAGCTATATGTTTCAGTTCCAGCCC 240

Qy 241 ATTGACTTGAATTTGTGGATGAACCATCAGAAGATGGTGGACAAACAAAGATTGAGATT 300
Db 241 ATTGACTTGAATTTGTGGATGAACCATCAGAAGATGGTGGACAAACAAAGATTGAGATT 300

Qy 301 AGCATGGAATGTATCCGATGACAGACTCGGACCTGAGTGAACCCCATGTGGCCACAGTAC 360
Db 301 AGCATGGAATGTATCCGATGACAGACTCGGACCTGAGTGAACCCCATGTGGCCACAGTAC 360

Qy 361 ACGRACCTGGGGCTCCTCAACAGCATGGACACAGAGATTTCAGAACGGCTCCTCGTCCACC 420
Db 361 ACGRACCTGGGGCTCCTCAACAGCATGGACACAGAGATTTCAGAACGGCTCCTCGTCCACC 420

Qy 421 AGTCCCTATACACAGACACACGCGCAAGACAGCGTCAGGGGCGCCCTCGCCCTTACGCACAG 480

RESULT 8

US-09-542-615A-332

; Sequence 332, Application US/09542615A

; Patent No. 6518256

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

```

; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-332

Query Match      48.9%; Score 1376; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTTGATATCAAGACAGTGTGAAGAAATGAATTTTGAACCTTCACGGTGTGCCACCT 60
Db 1 TCGTTGATATCAAGACAGTGTGAAGAAATGAATTTTGAACCTTCACGGTGTGCCACCT 60

Qy 61 ACAGTACTGCCCTGACCCCTTACATCCAGGTTTCGTAGAAACCCAGCTCATTTCTCTGG 120
Db 61 ACAGTACTGCCCTGACCCCTTACATCCAGGTTTCGTAGAAACCCAGCTCATTTCTCTGG 120

Qy 121 AAAGAAAGTTATTACCGATCCACCATGTCACAGACACACAGACAAATGAATTCCTCAGT 180
Db 121 AAAGAAAGTTATTACCGATCCACCATGTCACAGACACACAGACAAATGAATTCCTCAGT 180

Qy 181 CCAGAGGTTTCCAGCATATCTGGATTTCTGGAACAGCCTATATGTTTCAGTTCAGCCC 240
Db 181 CCAGAGGTTTCCAGCATATCTGGATTTCTGGAACAGCCTATATGTTTCAGTTCAGCCC 240

Qy 241 ATTGACTTGAATTTGTGGATGAACCATCAGAAGATGGTGGACAAAACAAGATTGAGATT 300
Db 241 ATTGACTTGAATTTGTGGATGAACCATCAGAAGATGGTGGACAAAACAAGATTGAGATT 300

Qy 301 AGCATGGACTGTATCCGATCAGACCTCGGACCTGAGTGACCCCATGTGCCACAGTAC 360
Db 301 AGCATGGACTGTATCCGATCAGACCTCGGACCTGAGTGACCCCATGTGCCACAGTAC 360

Qy 361 ACAGACCTGGGGCTCCTGAACAGCATGACACAGAGATTGAGACGGCTCTCTGTCACCC 420
Db 361 ACAGACCTGGGGCTCCTGAACAGCATGACACAGAGATTGAGACGGCTCTCTGTCACCC 420

Qy 421 AGTCCCTATAACACAGACACCGCAGAACAGCGTACGGGCGCTCTGCGCCCTACGCACAG 480
Db 421 AGTCCCTATAACACAGACACCGCAGAACAGCGTACGGGCGCTCTGCGCCCTACGCACAG 480

Qy 481 CCCAGCTCCAGCTTCGATGCTCTCTCTCATCACCAGGCGCATCCCTCCAAACCGACTAC 540
Db 481 CCCAGCTCCAGCTTCGATGCTCTCTCTCATCACCAGGCGCATCCCTCCAAACCGACTAC 540

Qy 541 CCAGCGCCGACAGTTTCAGCTGTCCTTCAGAGAGTGCAGACCGCCCAAGTCGGCCACC 600
Db 541 CCAGCGCCGACAGTTTCAGCTGTCCTTCAGAGAGTGCAGACCGCCCAAGTCGGCCACC 600

Qy 601 TGGAGCTATTCCACTGAACTGAAGAAATCTTACTGCCAAATTTGAAAAGACATGCCCCATC 660
Db 601 TGGAGCTATTCCACTGAACTGAAGAAATCTTACTGCCAAATTTGAAAAGACATGCCCCATC 660

Qy 661 CAGATCAAGGTGATGACCCCACTCTCTCAGGAGCTGTTATCCGCGCCATGCTGTCTAC 720
Db 661 CAGATCAAGGTGATGACCCCACTCTCTCAGGAGCTGTTATCCGCGCCATGCTGTCTAC 720

Qy 721 AAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
Db 721 AAAAAGCTGAGCAGCTCAGGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780

Qy 781 GAAATTCACAGGGGACAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC 840
Db 781 GAAATTCACAGGGGACAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC 840

Db 781 GAATTCACAGGGGACAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC 840
Qy 841 CATGCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGCTGCTACCTTATGAG 900
Db 841 CATGCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGCTGCTACCTTATGAG 900
Qy 901 CCACCCAGGTTGGCAGTGAATTCACGACAGTCTTGTACAATTTTCAATTTTCAATTTTCA 960
Db 901 CCACCCAGGTTGGCAGTGAATTCACGACAGTCTTGTACAATTTTCAATTTTCAATTTTCA 960
Qy 961 TGTGTTGGAGGATGAACCCGCTCCAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1020
Db 961 TGTGTTGGAGGATGAACCCGCTCCAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1020
Qy 1021 GGGCAAGTCTCTGGCCGACCGCTGCTTTGAGCCCGGATCTGCTGTTGCCAGGAAGAGAC 1080
Db 1021 GGGCAAGTCTCTGGCCGACCGCTGCTTTGAGCCCGGATCTGCTGTTGCCAGGAAGAGAC 1080
Qy 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT 1140
Db 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT 1140
Qy 1141 GATGTCAGGAGCCCGCTTTTCGTGAGAACACATGATGATCCAGATCAGATCCATCAAG 1200
Db 1141 GATGTCAGGAGCCCGCTTTTCGTGAGAACACATGATGATCCAGATCAGATCCATCAAG 1200
Qy 1201 AAACGAAGATCCCGAGATGATGAATCTGTTACTTATCCAGTGAGGGCGGTGAGACTTAT 1260
Db 1201 AAACGAAGATCCCGAGATGATGAATCTGTTACTTATCCAGTGAGGGCGGTGAGACTTAT 1260
Qy 1261 GAAATGCTGTTGAAAGATCAAAAGAGTCCCTGGAATCTCATGCACTACCTTCTCAGCACACA 1320
Db 1261 GAAATGCTGTTGAAAGATCAAAAGAGTCCCTGGAATCTCATGCACTACCTTCTCAGCACACA 1320
Qy 1321 ATTGAACAGTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376
Db 1321 ATTGAACAGTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376

RESULT 9
US-09-606-421B-332
; Sequence 332, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-332

Query Match      48.9%; Score 1376; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTTGATATCAAGACAGTGTGAAGAAATGAATTTTGAACCTTCACGGTGTGCCACCT 60
Db 1 TCGTTGATATCAAGACAGTGTGAAGAAATGAATTTTGAACCTTCACGGTGTGCCACCT 60
```

```
QY 61 ACAGTACTGCGCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
Db 61 ACAGTACTGCGCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
QY 121 AAAGAAAGTTATTACCGATCCACCATGTCAGAGCAGACAGACAAATGAATTCCTCAGT 180
Db 121 AAAGAAAGTTATTACCGATCCACCATGTCAGAGCAGACAGACAAATGAATTCCTCAGT 180
QY 181 CCAGAGTTTTCAGCATATCTGGGATTTTCGAAACAGCCTATATGTTGAGTTTCAGCCC 240
Db 181 CCAGAGTTTTCAGCATATCTGGGATTTTCGAAACAGCCTATATGTTGAGTTTCAGCCC 240
QY 241 ATTGACTTGAATCTTGTGATGAACCATCAAGATGTTGCGACAAACAGATTGAGATT 300
Db 241 ATTGACTTGAATCTTGTGATGAACCATCAAGATGTTGCGACAAACAGATTGAGATT 300
QY 301 AGCATGACTGTATCCGATCAGGACTCGGACCTGAGTGAACCCCATGTCGCCACAGTAC 360
Db 301 AGCATGACTGTATCCGATCAGGACTCGGACCTGAGTGAACCCCATGTCGCCACAGTAC 360
QY 361 ACAGAACTGGGGCTCCTGAACAGCATGGACCCAGAGATTGAGACGGCTCCTGCTCCACC 420
Db 361 ACAGAACTGGGGCTCCTGAACAGCATGGACCCAGAGATTGAGACGGCTCCTGCTCCACC 420
QY 421 AGTCCCTATTACACAGACACCGCAGAAACAGCGTCAAGCGCCCTCGCCCTACGACAG 480
Db 421 AGTCCCTATTACACAGACACCGCAGAAACAGCGTCAAGCGCCCTCGCCCTACGACAG 480
QY 481 CCCAGCTCCACCTTCGATGCTCTCTCCATCAACCCGCCATCCCTCCAAACACGACTAC 540
Db 481 CCCAGCTCCACCTTCGATGCTCTCTCCATCAACCCGCCATCCCTCCAAACACGACTAC 540
QY 541 CCAGGCCGACAGATTTCGAGCTGCTCTCCAGCAGTCGACGACGGCCCAAGTCGGCCACC 600
Db 541 CCAGGCCGACAGATTTCGAGCTGCTCTCCAGCAGTCGACGACGGCCCAAGTCGGCCACC 600
QY 601 TGGACGTTATCCACTGAACAACTCTACTGCCAAATTTGAAAGACATGCCCCATC 660
Db 601 TGGACGTTATCCACTGAACAACTCTACTGCCAAATTTGAAAGACATGCCCCATC 660
QY 661 CAGATCAAGGTATGACCCCACTCCTCAGGAGCTGTTATCCGCGCATGCTGTCTAC 720
Db 661 CAGATCAAGGTATGACCCCACTCCTCAGGAGCTGTTATCCGCGCATGCTGTCTAC 720
QY 721 AAAAAGCTGACGACGTACGAGGCTGTTGAGCGGTGAGCGGTGCCCCACCATGAGCCGT 780
Db 721 AAAAAGCTGACGACGTACGAGGCTGTTGAGCGGTGAGCGGTGCCCCACCATGAGCCGT 780
QY 781 GAATTTCAACGAGGACAGATTGCCCTCCTAGTCAATTTGATTTCGAGTAGAGGGGAAACAGC 840
Db 781 GAATTTCAACGAGGACAGATTGCCCTCCTAGTCAATTTGATTTCGAGTAGAGGGGAAACAGC 840
QY 841 CATGCCAGTATGTAAGATGCCATCAAGGAAAGACAGAGTGTGCTGTTACCTTATGAG 900
Db 841 CATGCCAGTATGTAAGATGCCATCAAGGAAAGACAGAGTGTGCTGTTACCTTATGAG 900
QY 901 CCACCCAGGTTGACACTGAATTCAGCAGCTCTTGTACAAATTTTCATGTTTACAGCAGT 960
Db 901 CCACCCAGGTTGACACTGAATTCAGCAGCTCTTGTACAAATTTTCATGTTTACAGCAGT 960
QY 961 TGTGTTGAGGGATGAACCGCGTCCAAATTTAATCATTTGTTACTCTGGAAACAGAGAT 1020
Db 961 TGTGTTGAGGGATGAACCGCGTCCAAATTTAATCATTTGTTACTCTGGAAACAGAGAT 1020
QY 1021 GGGCAAGTCTTGGGCCGACGCTGTTTGGGCCCGGATCTGTGCTTCCCGAGGAGAGAC 1080
Db 1021 GGGCAAGTCTTGGGCCGACGCTGTTTGGGCCCGGATCTGTGCTTCCCGAGGAGAGAC 1080
QY 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGACAGCAAGTTTCGGACAGTACAAAGACGGT 1140
Db 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGACAGCAAGTTTCGGACAGTACAAAGACGGT 1140
```

```
QY 1141 GATGTACGAAGCGCCGTTTCGTGAGAAACACACATGGTATCCAGATGACATCCATCAAG 1200
Db 1141 GATGTACGAAGCGCCGTTTCGTGAGAAACACACATGGTATCCAGATGACATCCATCAAG 1200
QY 1201 AAACGAAGATCCCGAGATGATGAATCTGTTATCTTACCATGAGGGCCGTGAGACTTAT 1260
Db 1201 AAACGAAGATCCCGAGATGATGAATCTGTTATCTTACCATGAGGGCCGTGAGACTTAT 1260
QY 1261 GAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCGTACCTTCTCTCAGCACACA 1320
Db 1261 GAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCGTACCTTCTCTCAGCACACA 1320
QY 1321 ATTGAAACGTACAGGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1376
Db 1321 ATTGAAACGTACAGGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1376

RESULT 10
US-09-630-940B-332
; Sequence 332, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C10
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-332

Query Match 48.9%; Score 1376; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTTGATATCAAGACAGTTGAAGGAAATGAATTTTGAACCTTCACGGTGTGCCACCT 60
Db 1 TCCTTGATATCAAGACAGTTGAAGGAAATGAATTTTGAACCTTCACGGTGTGCCACCT 60
QY 61 ACAGTACTGCGCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
Db 61 ACAGTACTGCGCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
QY 121 AAAGAAAGTTATTACCGATCCACCATGTCAGAGCAGACAGACAAATGAATTCCTCAGT 180
Db 121 AAAGAAAGTTATTACCGATCCACCATGTCAGAGCAGACAGACAAATGAATTCCTCAGT 180
QY 181 CCAGAGTTTTCAGCATATCTGGGATTTTCGAAACAGCCTATATGTTGAGTTTCAGCCC 240
Db 181 CCAGAGTTTTCAGCATATCTGGGATTTTCGAAACAGCCTATATGTTGAGTTTCAGCCC 240
QY 241 ATTGACTTGAATCTTGTGATGAACCATCAAGATGTTGCGACAAACAGATTGAGATT 300
Db 241 ATTGACTTGAATCTTGTGATGAACCATCAAGATGTTGCGACAAACAGATTGAGATT 300
QY 301 AGCATGACTGTATCCGATCAGGACTCGGACCTGAGTGAACCCCATGTCGCCACAGTAC 360
Db 301 AGCATGACTGTATCCGATCAGGACTCGGACCTGAGTGAACCCCATGTCGCCACAGTAC 360
```

```
QY 361 ACGAACCTGGGCTCCTGAACAGCATGGACAGAGATTGAGAACGGCTCCTCGTCCACC 420
Db 361 ACGAACCTGGGCTCCTGAACAGCATGGACAGAGATTGAGAACGGCTCCTCGTCCACC 420
QY 421 AGTCCCTATAACACAGACACACGGCGAGAACAGCGTCAACGGCGCCTCGCCCTACGACAG 480
Db 421 AGTCCCTATAACACAGACACACGGCGAGAACAGCGTCAACGGCGCCTCGCCCTACGACAG 480
QY 481 CCCAGTCCACCTTCGATGCTCTCTCCATCACCGGCCATCGCCCTCGAACCGGACTAC 540
Db 481 CCCAGTCCACCTTCGATGCTCTCTCCATCACCGGCCATCGCCCTCGAACCGGACTAC 540
QY 541 CCAGGCCCGCACAGTTTCCACGCTGCTCTTCCAGCAGTCAGACACCGCCCAAGTCGGCCACC 600
Db 541 CCAGGCCCGCACAGTTTCCAGCAGTCCTTCCAGCAGTCAGACACCGCCCAAGTCGGCCACC 600
QY 601 TGGACGTATTCCACTGAACCTGAAGAACTCTACTGCCAAATTCGCAAGACATGCCCCATC 660
Db 601 TGGACGTATTCCACTGAACCTGAAGAACTCTACTGCCAAATTCGCAAGACATGCCCCATC 660
QY 661 CAGATCAAGGTGATGACCCCACTCTCAGGGAGCTGTTATCGCGCCATGCTGTCTAC 720
Db 661 CAGATCAAGGTGATGACCCCACTCTCAGGGAGCTGTTATCGCGCCATGCTGTCTAC 720
QY 721 AAAAAAGCTGAGCACGTACGGAGTGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
Db 721 AAAAAAGCTGAGCACGTACGGAGTGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
QY 781 GAATTTCAACAGGGACAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC 840
Db 781 GAATTTCAACAGGGACAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC 840
QY 841 CATGCCAGTATGTAGAAGATCCCATCACAGGAGACAGAGTGTGCTGTACTTATGAG 900
Db 841 CATGCCAGTATGTAGAAGATCCCATCACAGGAGACAGAGTGTGCTGTACTTATGAG 900
QY 901 CCACCCAGGTTGGCACTCAATTCACGACAGTCTGTACAAATTTCAATGTTAACAGCAGT 960
Db 901 CCACCCAGGTTGGCACTCAATTCACGACAGTCTGTACAAATTTCAATGTTAACAGCAGT 960
QY 961 TGTGTTGAGGAGTGAACCGCGTCCAAATTTTAATCAATTTGTTACTCGGAAACCGAGAT 1020
Db 961 TGTGTTGAGGAGTGAACCGCGTCCAAATTTTAATCAATTTGTTACTCGGAAACCGAGAT 1020
QY 1021 GGGCAAGTCTGGGCCGACGCTGCTTTGAGGCCGAGATCTGTGCTTGGCCAGGAGAGAC 1080
Db 1021 GGGCAAGTCTGGGCCGACGCTGCTTTGAGGCCGAGATCTGTGCTTGGCCAGGAGAGAC 1080
QY 1081 AGGAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACACAGTACAAAGAACGTT 1140
Db 1081 AGGAGGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACACAGTACAAAGAACGTT 1140
QY 1141 GATGTTACGAAGCGCCGTTTCTGTCAGAAACACACATGATCCAGATGACATCCATCAAG 1200
Db 1141 GATGTTACGAAGCGCCGTTTCTGTCAGAAACACACATGATCCAGATGACATCCATCAAG 1200
QY 1201 AAACGAAGATCCCGAGATGATGAATCTGTTATACCTACAGTGAAGGGCGGTGAGACTTAT 1260
Db 1201 AAACGAAGATCCCGAGATGATGAATCTGTTATACCTACAGTGAAGGGCGGTGAGACTTAT 1260
QY 1261 GAATGCTCTGAGATCAAGAGTCCCTGGAATCATGACGATCCATGACGATCCCTGAGCAACA 1320
Db 1261 GAATGCTCTGAGATCAAGAGTCCCTGGAATCATGACGATCCATGACGATCCCTGAGCAACA 1320
QY 1321 ATTGAACCTGACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1376
Db 1321 ATTGAACCTGACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1376
```

RESULT 11

US-09-643-597-335

; Sequence 335, Application US/09643597

```
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Pan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-643-597-335
```

```
Query Match 48.4%; Score 1364; DB 3; Length 4849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1375; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 2 CGTTGATATCAAAGACAGTTGAAGAAATGAATTTTGAATTCACGGTGTGCCACCTTA 61
Db 1 CGTTGATATCAAAGACAGTTGAAGAAATGAATTTTGAATTCACGGTGTGCCACCTTA 60
QY 62 CAGTACTGCCCTGACCTTACATCCAGCGTTTCGTAGAAA-CCCAGCTCATTTCTCTTG 120
Db 61 CAGTACTGCCCTGACCTTACATCCAGCGTTTCGTAGAAAACCCAGCTCATTTCTCTTG 120
QY 121 AAGAAAGTTATTACCGATCCACCATGTCACAGAGACACAGACAAATTCCTCAGT 180
Db 121 AAGAAAGTTATTACCGATCCACCATGTCACAGAGACACAGACAAATTCCTCAGT 180
QY 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAAGTTCAGCCC 240
Db 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAACAGCCTATATGTTCAAGTTCAGCCC 240
QY 241 ATTGACTGAATTTGTGGATCAACCATCAGAGATGTTGCGACAAACAGATTTGAGATT 300
Db 241 ATTGACTGAATTTGTGGATCAACCATCAGAGATGTTGCGACAAACAGATTTGAGATT 300
QY 301 AGCATGGACTGTATCCGATCGAGACTCGGACCTGAGTGAGCCCATGTGGCCACAGTAC 360
Db 301 AGCATGGACTGTATCCGATCGAGACTCGGACCTGAGTGAGCCCATGTGGCCACAGTAC 360
QY 361 ACGAACCTGGGCTCCTGAACAGCATGGACAGAGATTGAGAACGGCTCCTCGTCCACC 420
Db 361 ACGAACCTGGGCTCCTGAACAGCATGGACAGAGATTGAGAACGGCTCCTCGTCCACC 420
QY 421 AGTCCCTATAACACAGACACACGGCGAGAACAGCGTCAACGGCGCCTCGCCCTACGACAG 480
Db 421 AGTCCCTATAACACAGACACACGGCGAGAACAGCGTCAACGGCGCCTCGCCCTACGACAG 480
QY 481 CCCAGTCCACCTTCGATGCTCTCTCCATCACCGGCCATCGCCCTCGAACCGGACTAC 540
Db 481 CCCAGTCCACCTTCGATGCTCTCTCCATCACCGGCCATCGCCCTCGAACCGGACTAC 540
QY 541 CCAGGCCCGCACAGTTTCCACGCTGCTCTTCCAGCAGTCAGACACCGCCCAAGTCGGCCACC 600
Db 541 CCAGGCCCGCACAGTTTCCACGCTGCTCTTCCAGCAGTCAGACACCGCCCAAGTCGGCCACC 600
QY 601 TGGACGTATTCCACTGAACCTGAAGAACTCTACTGCCAAATTCGCAAGACATGCCCCATC 660
Db 601 TGGACGTATTCCACTGAACCTGAAGAACTCTACTGCCAAATTCGCAAGACATGCCCCATC 660
```

Qy	661	CAGATCAAGG	TGATGA	CCCCAC	CTCTCT	CAGGAG	CTGTTAT	TCGCGG	CAATGC	CTGTCTAC	720
Db	661	CAGATCAAGG	TGATGA	CCCCAC	CTCTCT	CAGGAG	CTGTTAT	TCGCGG	CAATGC	CTGTCTAC	720
Qy	721	AAAAAAGC	TGAGCAG	CTCAGG	AGGTGGT	GAAAGCGG	TGCCCCAA	CCACCATG	AGCTGAG	CAGCCGT	780
Db	721	AAAAAAGC	TGAGCAG	CTCAGG	AGGTGGT	GAAAGCGG	TGCCCCAA	CCACCATG	AGCTGAG	CAGCCGT	780
Qy	781	GAATTTCA	ACGAGG	GACAGAT	TGCCCTCT	CTAGTCA	TTTTGA	TTTCAG	TAGAGG	GGAACAGC	840
Db	781	GAATTTCA	ACGAGG	GACAGAT	TGCCCTCT	CTAGTCA	TTTTGA	TTTCAG	TAGAGG	GGAACAGC	840
Qy	841	CATGCCAG	TATGTAG	AGATGCC	ATCACG	GRAGACAG	AGTGTC	TGTAC	CTTATG	AG	900
Db	841	CATGCCAG	TATGTAG	AGATGCC	ATCACG	GRAGACAG	AGTGTC	TGTAC	CTTATG	AG	900
Qy	901	CCACCCCA	GGTGGC	ACTG	AATTCAC	GACAGCTCT	TGTACA	ATTTCA	TGTGTGA	ACAGCAGT	960
Db	901	CCACCCCA	GGTGGC	ACTG	AATTCAC	GACAGCTCT	TGTACA	ATTTCA	TGTGTGA	ACAGCAGT	960
Qy	961	TGTGTTGG	AGGGATGA	ACCGCG	TCCAA	TTTTTA	TCA	TGTTACT	CTCGG	AAACAGAGAT	1020
Db	961	TGTGTTGG	AGGGATGA	ACCGCG	TCCAA	TTTTTA	TCA	TGTTACT	CTCGG	AAACAGAGAT	1020
Qy	1021	GGGCAAGT	CTCTGG	CGCAGC	GTCTTTG	AGSCCGG	ATCTGTG	CTCTCC	CAGGAAG	AGAC	1080
Db	1021	GGGCAAGT	CTCTGG	CGCAGC	GTCTTTG	AGSCCGG	ATCTGTG	CTCTCC	CAGGAAG	AGAC	1080
Qy	1081	AGGAAGCG	GGATGA	AGATAG	ATCAG	AAAGCAG	CAAGTTTC	CGGAC	AGTACAA	AGAACGGT	1140
Db	1081	AGGAAGCG	GGATGA	AGATAG	ATCAG	AAAGCAG	CAAGTTTC	CGGAC	AGTACAA	AGAACGGT	1140
Qy	1141	GATGTCAG	GAAGCCCG	CTTTT	CGTCAG	AACACATG	GTATCC	AGATG	ACATCC	ATCAAG	1200
Db	1141	GATGTCAG	GAAGCCCG	CTTTT	CGTCAG	AACACATG	GTATCC	AGATG	ACATCC	ATCAAG	1200
Qy	1201	AAACGAAG	ATCCCAG	ATGATGA	ACTGTTAT	TACTTAC	TGAGG	GGCCGTG	AGACTTAT		1260
Db	1201	AAACGAAG	ATCCCAG	ATGATGA	ACTGTTAT	TACTTAC	TGAGG	GGCCGTG	AGACTTAT		1260
Qy	1261	GAATGCTG	TGTAAGAT	CA	AAGAGTCC	TGGA	ACTCATG	CAGTAC	CTTCTC	CAGCACAC	1320
Db	1261	GAATGCTG	TGTAAGAT	CA	AAGAGTCC	TGGA	ACTCATG	CAGTAC	CTTCTC	CAGCACAC	1320
Qy	1321	ATTGAAAC	CGTACAGG	CAACAG	CAACAG	CAAGCAG	CACTTACTT	CA	AGAAACA		1376
Db	1321	ATTGAAAC	CGTACAGG	CAACAG	CAACAG	CAAGCAG	CACTTACTT	CA	AGAAACA		1376

RESULT 12

```

US-09-542-615A-335
; Sequence 335, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-335

```


QY 1021 GGCAGAGTCTGGGCGGAGCGCTCTTTGAGGCCCGGATCTGTCTTGGCCCGAGGAGAG 1080
Db 1021 GGGCAAGTCTGGGCGGAGCGCTCTTTGAGGCCCGGATCTGTCTTGGCCCGAGGAGAG 1080
QY 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGAGACAGTACAAAGACGGT 1140
Db 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGAGACAGTACAAAGACGGT 1140
QY 1141 GATGGTACGAAGCGCCGCTTTCTGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
Db 1141 GATGGTACGAAGCGCCGCTTTCTGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
QY 1201 AAACGAAGTCCCGAGATGATGAATCTTTATCTTACCAAGTGGGGCCGTCAGACTTAT 1260
Db 1201 AAACGAAGTCCCGAGATGATGAATCTTTATCTTACCAAGTGGGGCCGTCAGACTTAT 1260
QY 1261 GAAATGCTGTGAAGATCAAGAGTCCCTGGAATCTATGCAAGTACCTTCTCAGCACACA 1320
Db 1261 GAAATGCTGTGAAGATCAAGAGTCCCTGGAATCTATGCAAGTACCTTCTCAGCACACA 1320
QY 1321 ATTGAACGTTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376
Db 1321 ATTGAACGTTACAGGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376

RESULT 13

US-09-606-421B-335
; Sequence 335, Application US/09606421B
; Patent No. 653135

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 335

; LENGTH: 4849

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-606-421B-335

Query Match 48.4%; Score 1364; DB 4; Length 4849;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1375; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 CGTTGATATCAAGACAGTTGAAGGAATGAATTTTGAACCTTTCACGGGTGCGCCCTTA 61
Db 1 CGTTGATATCAAGACAGTTGAAGGAATGAATTTTGAACCTTTCACGGGTGCGCCCTTA 60
QY 62 CAGTACTGCCCTGACCTTTACATCCAGCGTTTCGTAGAAA-CCCAAGCTATTCTCTGG 120
Db 61 CAGTACTGCCCTGACCTTTACATCCAGCGTTTCGTAGAAA-CCCAAGCTATTCTCTGG 120
QY 121 AAAGAAAGTTATACCGATCCACCATGTCCTCAGAGACACAGACAAATGAATTCCTCAGT 180
Db 121 AAAGAAAGTTATACCGATCCACCATGTCCTCAGAGACACAGACAAATGAATTCCTCAGT 180
QY 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGACAGCTATATGTTTCAGTTGAGCCC 240
Db 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGACAGCTATATGTTTCAGTTGAGCCC 240
QY 241 ATTGACTTGAATCTTTGTGGATGAACCATCAGAAGATGGTGGCAGCAACAAAGATTGAGATT 300

Db 241 ATTGACTTGAATCTTTGTGGATGAACCATCAGAAGATGGTGGCAGCAACAAAGATTGAGATT 300
QY 301 ACGATGGAGTGTATCGGCATCGAGACTCGGACCTGAGTGAACCCCATGTGGCCACAGTAC 360
Db 301 ACGATGGAGTGTATCGGCATCGAGACTCGGACCTGAGTGAACCCCATGTGGCCACAGTAC 360
QY 361 ACGAACCTGGGGCTCTCTGAACAGCATGGACAGCAGATTTCAGAACGGCTCCTCGTCCACC 420
Db 361 ACGAACCTGGGGCTCTCTGAACAGCATGGACAGCAGATTTCAGAACGGCTCCTCGTCCACC 420
QY 421 AGTCCCTATTAACACAGACCAACCGCAGAAACAGGGTCAACGGCGCTTCGGCCCTACGACAG 480
Db 421 AGTCCCTATTAACACAGACCAACCGCAGAAACAGGGTCAACGGCGCTTCGGCCCTACGACAG 480
QY 481 CCCAGCTCCACCTTCGATGCTCTCTCCATCAGCCGCTATCCCTTCAACACCGACTAC 540
Db 481 CCCAGCTCCACCTTCGATGCTCTCTCCATCAGCCGCTATCCCTTCAACACCGACTAC 540
QY 541 CCAGGCCGCGACAGTTTCGACGCTGCTTCAGAGCAGTCGAGCACCGCCCAAGTCGGCCACC 600
Db 541 CCAGGCCGCGACAGTTTCGACGCTGCTTCAGAGCAGTCGAGCACCGCCCAAGTCGGCCACC 600
QY 601 TGGACGTTATTCACCTGAACCTGAAGAACTCTTACTGCCAAATTCGCAAGACATGCCCATC 660
Db 601 TGGACGTTATTCACCTGAACCTGAAGAACTCTTACTGCCAAATTCGCAAGACATGCCCATC 660
QY 661 CAGATCAAGGTTGATGACCCCACTCTCAGGGAGCTGTTATCCGCGCCATGCTGCTCTAC 720
Db 661 CAGATCAAGGTTGATGACCCCACTCTCAGGGAGCTGTTATCCGCGCCATGCTGCTCTAC 720
QY 721 AAAAAAGCTGAGCAGCTCACGGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
Db 721 AAAAAAGCTGAGCAGCTCACGGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
QY 781 GAAATCAACAGGAGCAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC 840
Db 781 GAAATCAACAGGAGCAGATTGCCCTCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC 840
QY 841 CATGCCAGTATGTAGAGATCCCATCAGGAAGACAGAGTGTGCTGCTACCTTATGAG 900
Db 841 CATGCCAGTATGTAGAGATCCCATCAGGAAGACAGAGTGTGCTGCTACCTTATGAG 900
QY 901 CCACCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAAATTTCAATGTGAACAGCAGT 960
Db 901 CCACCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAAATTTCAATGTGAACAGCAGT 960
QY 961 TGTGTTGAGGGATGAACCGCGCTCAATTTTAAATCAATTTGTTACTCTGGAACACAGAT 1020
Db 961 TGTGTTGAGGGATGAACCGCGCTCAATTTTAAATCAATTTGTTACTCTGGAACACAGAT 1020
QY 1021 GGGCAAGTCTGGCGGAGCGCTGTTGAGGCCCGGATCTGCTGTTGCCCGAGGAGAGAC 1080
Db 1021 GGGCAAGTCTGGCGGAGCGCTGTTGAGGCCCGGATCTGCTGTTGCCCGAGGAGAGAC 1080
QY 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGAGACAGTACAAAGACGGT 1140
Db 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGAGACAGTACAAAGACGGT 1140
QY 1141 GATGTAAGAGCGCGCTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
Db 1141 GATGTAAGAGCGCGCTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
QY 1201 AAACGAAGTCCCGAGATGATGAATCTTTATCTTACCAAGTGGGGCCGTCAGACTTAT 1260
Db 1201 AAACGAAGTCCCGAGATGATGAATCTTTATCTTACCAAGTGGGGCCGTCAGACTTAT 1260
QY 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCAAGTACCTTCTCAGCACACA 1320
Db 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTCATGCAAGTACCTTCTCAGCACACA 1320
QY 1321 ATTGAAACGTTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1376

Query Match	43.8%;	Score 1232;	DB 3;	Length 1551;
Best Local Similarity	100.0%;	Prod. No. 0;		
Matches 1232;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	145	ATGTCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG	204	
Db	1	ATGTCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG	60	
Qy	205	GATTTTCTGGAAACGCTATATGTTTCAGTTCAGGCCATTGACTTGAACCTTTGTGGATCAA	264	
Db	61	GATTTTCTGGAAACGCTATATGTTTCAGTTCAGGCCATTGACTTGAACCTTTGTGGATCAA	120	
Qy	265	CCATCAGAAGATGTGGCGACAAAACAAGATTAGATAGCATGGACTGTATCCGATGCG	324	
Db	121	CCATCAGAAGATGTGGCGACAAAACAAGATTAGATAGCATGGACTGTATCCGATGCG	180	
Qy	325	GACTCGAACCTGAGTGACCCCATGTGGCCACAGTACAGAACCTGGGGCTCTGAAACGC	384	
Db	181	GACTCGAACCTGAGTGACCCCATGTGGCCACAGTACAGAACCTGGGGCTCTGAAACGC	240	
Qy	385	ATGGACCAGCAGATTTCAGAACGGCTCTCTGTCACCACTCCCTCTATAACACAGACCAAGCG	444	
Db	241	ATGGACCAGCAGATTTCAGAACGGCTCTCTGTCACCACTCCCTCTATAACACAGACCAAGCG	300	
Qy	445	CAGAACAGCGTACGGCGCCCTCGCCCTTACGCAACAGCCAGCTCACTTCGATGCTCTC	504	
Db	301	CAGAACAGCGTACGGCGCCCTCGCCCTTACGCAACAGCCAGCTCACTTCGATGCTCTC	360	
Qy	505	TCCTCATACCCGCGCATCCCTCCAAACACGACTACCCAGGCCGACAGTTTCGACGCTG	564	
Db	361	TCCTCATACCCGCGCATCCCTCCAAACACGACTACCCAGGCCGACAGTTTCGACGCTG	420	
Qy	565	TCCTTCCAGCAGTGCAGCACCGCCAAAGTCGGCCACCTGGAGCGTATTCACATGAACCTGAAG	624	
Db	421	TCCTTCCAGCAGTGCAGCACCGCCAAAGTCGGCCACCTGGAGCGTATTCACATGAACCTGAAG	480	
Qy	625	AAACTCTACTGCCAAATTTGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACT	684	
Db	481	AAACTCTACTGCCAAATTTGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACT	540	
Qy	685	CCTCAGGGAGCTGTTATCCGGCCCATGCGCTGTCTACAAAAGCTGAGCAGCTCACGGAG	744	
Db	541	CCTCAGGGAGCTGTTATCCGGCCCATGCGCTGTCTACAAAAGCTGAGCAGCTCACGGAG	600	
Qy	745	GTGGTGAAGCGTGCCCAACCATGAGTGCAGCGTGAATTCACAGGGGACAGATTGCC	804	
Db	601	GTGGTGAAGCGTGCCCAACCATGAGTGCAGCGTGAATTCACAGGGGACAGATTGCC	660	
Qy	805	CCTCCTAGTCATTTGATTCGAGTAGAGGGGAACGCCATGCCAGTATGTAGAAGATCCC	864	
Db	661	CCTCCTAGTCATTTGATTCGAGTAGAGGGGAACGCCATGCCAGTATGTAGAAGATCCC	720	
Qy	865	ATCACAGGAAGACAGATGTGCTGGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC	924	
Db	721	ATCACAGGAAGACAGATGTGCTGGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC	780	
Qy	925	ACGACAGTCTTGTAACAATTTTCATGTGTAAACAGCAGTTGTGTGGAGGGATCAACCGCGT	984	
Db	781	ACGACAGTCTTGTAACAATTTTCATGTGTAAACAGCAGTTGTGTGGAGGGATCAACCGCGT	840	
Qy	985	CCAATTTTAATCATTTGTTACTCTCTGGAAACACAGAGATGGGCAAGTCTCTGGGCCGACGCTG	1044	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 3, 2005, 06:01:58 ; Search time 936 Seconds
(without alignments)
3304.793 Million cell updates/sec.
Title: US-09-670-568C-1
Perfect score: 2383
Sequence: 1 MSQSTQTNFLSPVFOH.....PKQSDVFFRHKKPPNRVYP 448

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09670568/runat_03102005_070152_24348/app_query.fasta_1.647
-DB=Published Applications NA -QMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09670568 @CEN 1.1.832 @runat 03102005_070152_24348
-NCFU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2383	100.0	1347	19	US-10-716-359-3
2	2383	100.0	2816	9	US-09-735-705-333
3	2383	100.0	2816	9	US-09-850-716A-333
4	2383	100.0	2816	9	US-09-897-778-333
5	2383	100.0	2816	14	US-10-007-700-333
6	2383	100.0	2816	15	US-10-117-982-333
7	2383	100.0	2816	16	US-10-393-590-26
8	2383	100.0	2816	16	US-10-393-590-27
9	2383	100.0	2816	16	US-10-393-590-64
10	2383	100.0	2816	16	US-10-393-590-65
11	2383	100.0	2816	16	US-10-393-567-26
12	2383	100.0	2816	16	US-10-393-567-27
13	2383	100.0	2816	16	US-10-393-567-64
14	2383	100.0	2816	16	US-10-393-567-65
15	2383	100.0	2816	16	US-10-394-087-26
16	2383	100.0	2816	16	US-10-394-087-27
17	2383	100.0	2816	16	US-10-394-087-64
18	2383	100.0	2816	16	US-10-394-087-65
19	2383	100.0	2816	17	US-10-313-986-333
20	2383	100.0	2816	20	US-10-775-972-333
21	2383	100.0	2816	22	US-10-522-124-333
22	2296	96.3	1452	19	US-10-716-359-9
23	2185	91.7	1551	9	US-09-735-705-337
24	2185	91.7	1551	9	US-09-850-716A-337
25	2185	91.7	1551	9	US-09-897-778-337
26	2185	91.7	1551	14	US-10-007-700-337
27	2185	91.7	1551	15	US-10-117-982-337
28	2185	91.7	1551	17	US-10-313-986-337
29	2185	91.7	1551	19	US-10-716-359-2
30	2185	91.7	1551	20	US-10-775-972-337
31	2185	91.7	1551	22	US-10-522-124-337
32	2185	91.7	1926	19	US-10-716-359-1
33	2185	91.7	2270	9	US-09-735-705-332
34	2185	91.7	2270	9	US-09-850-716A-332
35	2185	91.7	2270	9	US-09-897-778-332
36	2185	91.7	2270	14	US-10-007-700-332
37	2185	91.7	2270	15	US-10-117-982-332
38	2185	91.7	2270	17	US-10-313-986-332
39	2185	91.7	2270	20	US-10-775-972-332
40	2185	91.7	2270	22	US-10-522-124-332
41	2185	91.7	4849	9	US-09-735-705-335
42	2185	91.7	4849	9	US-09-850-716A-335
43	2185	91.7	4849	9	US-09-897-778-335
44	2185	91.7	4849	14	US-10-007-700-335
45	2185	91.7	4849	15	US-10-117-982-335

ALIGNMENTS

RESULT 1
US-10-716-359-3
; Sequence 3, Application US/10716359
; Publication No. US2004013120A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Annie
; APPLICANT: McKeon, Frank
; TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
; FILE REFERENCE: HMV-038.01
; CURRENT APPLICATION NUMBER: US/10716.359
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: US/09/174,493
; PRIOR FILING DATE: 1998-10-15
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-05-29
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-29

;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/062,076

;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-15

;; NUMBER OF SEQ ID NOS: 50

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 3

;; LENGTH: 1347

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (1)..(1344)

US-10-716-359-3

Alignment Scores:

Pred. No.: 3,81e-277 Length: 1347
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-670-568C-1 (1-448) x US-10-716-359-3 (1-1347)

```
Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTyr 20
Db 1 ATGTCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCAGACATATCTGG 60
Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 61 GATTTCCTGGNACAGCCTATATGTTTCAGTTCAGGCCCATGACTTGAACTTTGTGGATGAA 120
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluLeuSerMetAspCysIleArgMetGln 60
Db 121 CCATCAGAAGATGTGGCACAACAAGATTAGCATTAGCATGGACTGTATCGCATGCAG 180
Qy 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 181 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACTTGGGGCTCCTGAAACAGC 240
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 241 ATGGACACGACGAGATTCAGAACGGCTCTCTGTCACACAGTCCCTATATACACAGACCG 300
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 301 CAGAACAGGTCACGGCGCCCTCGCCCTACGCACAGCCAGCTCCACCTTCGATGCTCTC 360
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 361 TCTCCATCACCCGCATCCCTCCCAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG 420
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
Db 421 TCCTTCAGCAGGTGACGACCGCCCAAGTCGCCACCTGGAGCTATTCACCTGAACCTGAG 480
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 481 AAACCTACTGCCAAATTCGAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCT 540
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 541 CCTCAGGAGGTGTTATCCGGCCCATGCTGTACAAAAAAGCTGAGCAGCTCAGCGAG 600
Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 601 GTGGTGAAGCGTGCCCAACCATGAGCTGAGCGCTGATTCACAGGAGGACAGATTGCC 660
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 661 CCTCCTAGTATTGATTTCGAGTAGAGGGGAACAGCCATGCCAGTATGTAGAAGATCCC 720
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
```

```
Db 721 ATCACAGGAAGACAGAGTGTGGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 780
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArg 280
Db 781 ACCACAGTCTTGTACAAATTCATGTGTAAACAGCAGTGTGTGGAGGGATGAACCGCGT 840
Qy 281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 841 CCAATTTTATCATTTGTTACTCTGGAAACCCAGAGATGGGCAAGTCTCTGGGCCGACGTGC 900
Qy 301 PheGluAlaArgIleCysAlaCysProGlyValArgAspArgLysAlaAspGluAspSerIle 320
Db 901 TTTGAGCCCCGATCTGTCTGCCAGGAAGACAGAGGCGGATGAAGATAGATC 960
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 961 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGTTACGAAGCCCGCTTCGT 1020
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1021 CAGAACACACATGTTATCCAGATGACATCCATCAAGAAACGAAGATCCCAGATGATGAA 1080
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1081 CTGTTATATCTTACAGTGGGGCCCGTGAGACCTTATGAATGCTGTGAAGATCAAGAG 1140
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1141 TCCTTGGAACTCATGTCAGTACCTTCTCAGCACACAAATGAAACGTACAGGCAACGAA 1200
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1201 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACATCTCTTCAGCCCTCTTCAGGAATGAG 1260
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1261 CTTGTGGAGCCCCGGAGAGAACTCCAAAACATCTGACGCTCTCTTTAGACATCCCAAG 1320
Qy 441 ProProAsnArgSerValTyrPro 448
Db 1321 CCCCCAAACCGATCAGTGTACCCA 1344
```

RESULT 2

US-09-735-705-333

;; Sequence 333, Application US/09735705

;; Patent No. US20020052329A1

;; GENERAL INFORMATION:

;; APPLICANT: Wang, Tongtong

;; APPLICANT: Fan, Liqun

;; APPLICANT: Kalos, Michael D.

;; APPLICANT: Bangur, Chaitanya S.

;; APPLICANT: Hosken, Nancy

;; APPLICANT: Fanger, Gary R.

;; APPLICANT: Li, Samuel X.

;; APPLICANT: Wang, Aijun

;; APPLICANT: Skeiky, Yasir A.W.

;; APPLICANT: Henderson, Robert A.

;; APPLICANT: McNeill, Patricia D.

;; APPLICANT: Fanger, Neil

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

;; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

;; FILE REFERENCE: 210121.455C14

;; CURRENT APPLICATION NUMBER: US/09/735,705

;; CURRENT FILING DATE: 2000-12-12

;; NUMBER OF SEQ ID NOS: 419

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 333

;; LENGTH: 2816

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-09-735-705-333

Alignment Scores:

Db 325 GACTCGGACCTGAGTACGCCCATGTGGCCACAGTACAGAACCTGGGGCTCCTGAACAGC 384
QY 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrThrProTyrAsnThrAspHisAla 100
Db 385 ATGACACGACAGATTCAAGCGGTCTCTGCTCCACCAAGTCCCTATAACACAGACCGCG 444
QY 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACAGCGTCACGGCGCCCTCCGCTACGACAGCCCGAGTCCACCTTCGATGCTCTC 504
QY 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCGGCATCCCTCCCAACACCGACTACCGACCGCCCGCAGCTTCGACGTG 564
QY 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db 565 TCCCTTCAGCAGTCCGACCGCCCAAGTCGGCCACCTGGACGTATTCCTACTGAAGTGAAG 624
QY 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACCTACTGCCAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCCACT 684
QY 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTATATCCGGCCATCGCTGTCTACAAAAAAGCTGAGCAGCTCACGGAG 744
QY 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGTGAAGCGTGAATTCACAGGAGGACAGATTGCC 804
QY 221 ProProSerHisLeuIleArgValGluGlyValGlnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CCTCCTAGTCTATTGTATCGAGTAGAGGGGAACAGCATCGCCAGTATGTAGAAGATCCC 864
QY 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCACAGAAAGACAGAGTGTGTGTGTTACCTATGAGCCACCCCGAGTGTGCAATTC 924
QY 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACACACGTCTGTACAAATTCATGTGTAAACAGCAGTGTGTGTGAGGGATGAACCGCCGT 984
QY 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 985 CCAATTTTATCATTTGTTACTCTGAAACCCAGAGATGGCGAAGTCTCTGGCCCGCAGCTGC 1044
QY 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGCCCGGATCTGTGCTTGCCAGGAAGACAGACAGGAAGCGGATGAAGATAGCATC 1104
QY 321 ArgLysGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGACGGTGTGTGTGAGAGCGCCCGTTTCGT 1164
QY 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGA 1224
QY 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysLysGlu 380
Db 1225 CTGTTATACTTACCAAGTGGAGGGCGGTGAGACTTATGAAATGTGTTGAAGATCAAGAG 1284
QY 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCCTGGAATCTATGACAGTACCTTCTCCAGACACAAATTTGAAACGTACAGGCAACAGCA 1344
QY 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGACCCAGCAGCTTACTTCAGAAACAATCTCTTTCCGCTGCTTCAGGAATGAG 1404
QY 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1405 CTTTGTGAGCCCCGGAGAGAAACTCCAAAAACAATCTGACGCTCTCTTTAGACATTTCAAAG 1464

QY 441 ProProAsnArgSerValTyrPro 448
Db 1465 CCCCCAACCGATCAGTGTACCCA 1488

RESULT 4

US-09-897-778-333
; Sequence 333, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-333

Alignment Scores:
Pred. No.: 1,216-276 Length: 2816
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-670-568C-1 (1-448) x US-09-897-778-333 (1-2816)

QY 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db 145 ATGTCCTCCAGACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCAGCATATCTGG 204
QY 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGAACAGCCTATATGTTTCAGTTACGCCCATTTGACCTTGTGGATGAA 264
QY 41 ProSerGluAspGlyValAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 265 CCATCAAGATGTGTGCGCAACAAAGATTGAGATTAGCATGGACTGTATCCGATGCGAG 324
QY 61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACTGGGGCTCCTGAAACAGC 384
QY 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGGACACAGCATTCAGAACCGCTCCCTCCAGCAGTCCCTTATAACACAGACCGCGG 444
QY 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACAGCGTTCAGGGCGCCCTCGCCCTACGACAGCCAGCTCCACCTTCGATGCTCTC 504
QY 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCGCCATCCCTCCAAACACCGACTACCCAGGCGCCGACAGTTTCGACGTG 564
QY 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db 565 TCCCTTCAGCAGTCCGACCGCCCAAGTCGGCCACCTGGACGCTATTTCCACTGAAGTGAAG 624

```
Qy 161 LysLeuTyrCysGlnAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACCTACTGCGCAAAATGCAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTTATCCGCGCATGCTGTCTACAAAAAAGCTGAGCAGCTCACGGAG 744
Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGTGAAGCGGTGCCCAACATGAGCTGAGCGTGAATTCACACGAGGGACAGATTGCC 804
Qy 221 ProProSerHisLeuIleArgValIleGluGlyAsnSerHisAlaGlnTyrValIleAspPro 240
Db 805 CCTCCTAGTCATTGATTGAGTGAAGGGAACAGCCATGCCCATGTATGTAGAGATCCC 864
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCACAGGAACAGAGAGTGTCTGTACCTTATGAGCCACCCAGGTTGGCACTGAAATTC 924
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACGACAGTCTGTGTACAAATTCATGTGTAAACAGCAGTTGTGTGGAGGGATGAACCGCGT 984
Qy 281 ProfileLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgCys 300
Db 985 CCATTTTATCATCTGTTACTCTGGAACACAGAGATGGGCAGTCTTGCGCCGACGTGC 1044
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCGAGTCTGTGCTGTGCCAGGAAGACAGAGGAGCGGATGAAGATAGCATC 1104
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGTGTATGTGTACGAAGCGCCGTTTCGT 1164
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGTATTCAGATGCATCCATCAAGAAACGAGATCCCCAGATGATGAA 1224
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1225 CTGTTATACTTACCAGTGAGGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAAAG 1284
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCTTGAACCTCATGTCAGTACTCTTCCTCAGCACACAATTGAACGTTACAGGCAACGCA 1344
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCAGCAGCAGCTTACTTTCAGAAACATCTCTTCAGCGCTGCTTCAGGAATGAG 1404
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1405 CTTGTGGAGCCCCGGAGAGAACTCCAAAACAATCTGACGCTCTCTTTAGACATTCCAAG 1464
Qy 441 ProProAsnArgSerValTyrPro 448
Db 1465 CCCCCAACCGATCAGTGTACCCA 1488
```

RESULT 5

```
US-10-007-700-333
; Sequence 333, Application US/10007700
; Publication No. US20030064947A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongcong
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
```

```
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cai, Feng
; APPLICANT: Roy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C17
; CURRENT APPLICATION NUMBER: US/10/007.700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-007-700-333

Alignment Scores:
Pred. No.: 1,21e-276 Length: 2816
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-670-568C-1 (1-448) x US-10-007-700-333 (1-2816)
```

```
Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db 145 ATGTCCAGAGCAGCACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG 204
Qy 21 AspPheLeuGluGlnProfileCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGAACAGCCTATATGTTTCAGTTTCAGCCCATTCAGTTGAACTTTGTGGATGA 264
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluLysSerMetAspCysIleArgMetGln 60
Db 265 CCATCAGAAGATGTCGCAACAAGATTGAGATTAGCATGAGCTGATCCGATGCGAG 324
Qy 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAAACAGC 384
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGACACAGCAGATTCAGAACGGCTCTCTGTCACACAGTCCCTATATACACAGACACGCG 444
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACAGCGTCAACGGCGCTCGCCCTACGACACAGCCAGCTCCACCTTCGATGCTCTC 504
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCCGCCATTCCTCCAAACACCGCATACCCAGCCGCGCAGCTTCGAGCGTG 564
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db 565 TCCTTCAGCAGTTCGAGCAGCCGCAAGTCGCCACCTCGAGCTATTCCATGAACTGAAG 624
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACCTACTGCGCAAAATGCAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTTATCCGCGCATGCTGTCTACAAAAAAGCTGAGCAGCTCACGGAG 744
```

```
Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGCTGAAGCGTCCCAACCATGAGCTGAGCGTGAATTCACACGAGGGACAGATTGCC 804

Qy 221 ProProSerHisLeuIleArgValGluClyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CCTCCTAGTCAATTTGATTGCGAGTAGAGGGGAACAGCCATGCCAGATGTAGAAAGATCCC 864

Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCACAGGAAGACAGAGTGTGCTGATACCTATGAGCCACCCAGGTTGGCACTGAATTC 924

Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACGACAGTCTTGTAACAATTTTCATGTAAACAGCAGTGTGTGTGGAGGGATCAACCGCGT 984

Qy 281 ProfileLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 985 CCAATTTTAAATCATGTTACTCTGGAACACAGAGATGGGCAAGTCTTGGGCCGACGCTGC 1044

Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCCGGATCTGTGCTTCCAGGAAGACACAGGAAGCGGATGAAGATAGATC 1104

Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAGCAGCAAGTTTCGACAGTACAAAGAACCGTGATGTGTACGAAGCGCCCGTTTCGT 1164

Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGTAGAA 1224

Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLysIleLysGlu 380
Db 1225 CTGTTATCTATCCAGTGAGGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAGAG 1284

Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCTGTGAATCTATGTCAGTACCTTCTCTCAGCACACAATTTGAACGTACAGGCAACAGCA 1344

Qy 401 GlnGlnGlnHisGlnHisLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCAGCAGCAGCAGTCTTCTCAGAAACATCTCTTTCAGCCTGCTTCAGAAATGAG 1404

Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1405 CTGTGTGAGCCCGGAGAGAACTCCAAACATCTGACGCTCTTTTAGACATTCACAG 1464

Qy 441 ProProAsnArgSerValTyrPro 448
Db 1465 CCCCCAACCGATCAGTGTACCCA 1488
```

RESULT 6

US-10-117-982-333

; Sequence 333, Application US/10117982

; Publication No. US20030138438A1

; GENERAL INFORMATION:

; APPLICANT: Foy, Teresa M.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedrick, Thomas S.

; APPLICANT: Carter, Darick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Mericle, Barbara

; APPLICANT: Spies, Gregory A.

; APPLICANT: Fan, Liqun

; APPLICANT: Wang, Tongtong

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C18

; CURRENT APPLICATION NUMBER: US/10/117,982

; CURRENT FILING DATE: 2002-04-05

```
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-117-982-333
```

Alignment Scores:

Pred. No.:	1-21e-276	Length:	2816
Score:	2383.00	Matches:	448
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-09-670-568C-1 (1-448) x US-10-117-982-333 (1-2816)

```
Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTyrp 20
Db 145 ATGTCCAGAGCAGACACAGAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG 204

Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGAAACAGCCTATATGTTGAGTTACGCCATTCAGCTTGAACTTTTGATGAA 264

Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 265 CCATCAGAAGATGGTGGCGAACAACAGATTGAGATTAGCATGACTGTATCCGCATGCAG 324

Qy 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCTCTGAACAGC 384

Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGGACACAGATTCAGAACCGCTCTCTGTCACCAAGTCCCTTATTAACACAGACACCGC 444

Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCAGCTCCACCTTCGATGCTCTC 504

Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCATCCCGCCATCCCTCCAAACACCGACTACCCAGGCCCGCACAGTTTCGACGTG 564

Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
Db 565 TCCTTCCAGCGTCCGAGCACCGCCAAAGTCGGCCACCTGGACGTTATTCCTGAACTGAAG 624

Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACCTACTGCCAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGAGCCCCACCT 684

Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTTATTCGCGCCATGCTCTGTCTACAAAAAAGCTGAGCAGCTCACGGAG 744

Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCCCAACCATGAGCTGAGCCGTGAATTCACCCAGGACAGATTGCC 804

Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CCTCTAGTCAATTTGATTGAGTAGAGGGGAAACAGCCATGCCAGTATGTAGAAGATCCC 864

Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCACAGGAAGACAGAGTGTGCTGTACCTTATGAGCCACCCAGGTTGGCATCTGAATTC 924

Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACGACAGTCTTTGTAACAATTTTCATGTAAACAGCAGCTGTGTGGAGGGATGAACCCCGT 984
```



```
Qy 281 ProfileLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgCys 300
Db 985 CCAATTTTAAATCAATTTACTCTGGAACACAGAGATGGCAAGTCTCTGGGCGGAGCTGC 1044
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCGCGAGTCTGTGCTTGGCCAGGAAGACAGGAAGGCGGATGAAGATAGCATC 1104
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAGCAGCAGCAAGTTTCGACAGTACAAAGAACCGTGATGTGTACGAAGCGCCCTTTTCGT 1164
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA 1224
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1225 CTGTTATACTTACCAGTGCAGGGCGCTGAGACTTATGAAATGCTGTGTTGAAGATCAAAAG 1284
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCCTGGAACCTCATGCAGTACCTTCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCACCAGCAGCTTACTTTCAGAAACATCTCTTTCAGGCTGCTTCAGGAATGAG 1404
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1405 CTTGTGGAGCGCCGAGAGAACTCCAAACAATCTGACGCTTCTTTTAGACATTTCCAAG 1464
Qy 441 ProProAsnArgSerValTyrPro 448
Db 1465 CCCCCAACCGATCAGTGTACCCA 1488

RESULT 7
US-10-393-590-26
; Sequence 26, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-590-26

Alignment Scores:
Pred. No.: 1,21e-276 Length: 2816
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-670-568C-1 (1-448) x US-10-393-590-26 (1-2816)

Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTyr 20
Db 145 ATGTCCAGAGCAGCACAGACAAATGAAATTCCTCAGTCCAGAGGTTTTCAGACATATCTGG 204
Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
|
```

```
Db 205 GATTTTTCGAAACAGCCCTATATGTTTCAGTTCAGCCCATTTGACTTTGAACTTTGTGGATGAA 264
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysValIleArgMetGln 60
|
Db 265 CCATCAGAGATGTTGGCGCAACAAAGATTGAGATTAGCATGGACTGTATCCGATGCGAG 324
Qy 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
|
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCTCGAACACAGC 384
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
|
Db 385 ATGGACACAGAGATTACAGACCGCTCTCGTCCACCATGCTCCCTATAACACACAGACACCGC 444
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
|
Db 445 CAGAACAGCTCAGGGCGCCCTCGCCCTACGACAGCCAGCTCCACTTCGATGCTCTC 504
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
|
Db 505 TCTCCATCACCGCCCATCCCTCCAAACACAGCTACCCAGCGCCGACAGTTTCGACGTG 564
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
|
Db 565 TCCTTCCAGCAGTCGAGCAGCCGCAAGTCGCGCCACCTGCGACGTATTCCTACTGAACCTGAAG 624
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
|
Db 625 AAATCTACTGTCGCAATTTGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCT 684
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
|
Db 685 CCTCAGGAGCTGTTATCGCGCCATGCTGTCTCAAAAAAAGCTGAGCAGCTCACGGAG 744
Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
|
Db 745 GTGTTGAAGCGGTGCCCAACCATGAGCTGAGCGCTGAAATTCACAGAGGACAGATGCCC 804
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
|
Db 805 CTTCTTAGTCAATTTGATTGAGTAGAGGGGAAACAGCCATGCCAGTATGTAGAGATCCC 864
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
|
Db 865 ATCACAGGAAGACAGAGTGTGCTGTGTTACCTTATGAGCCACCCAGGTGGCACTGAATTC 924
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
|
Db 925 ACGACAGTCTTGTACAAATTTTCATGTGTAAACAGCAGTGTGTGTTGAGGGGATGAACCGCGT 984
Qy 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyValArgCys 300
|
Db 985 CCAATTTTATCAATTTGTTACTCTGGAACCCAGAGATGGGCAAGTCTCTGGGCGGACGCTGC 1044
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
|
Db 1045 TTTGAGGCGCGGATCTGTGCTTCCCGCAGGAGACAGGAGCGGATGAAGATGATGATC 1104
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
|
Db 1105 AGAAGCAGCAGCAAGTTTCGACAGTACAAAGAACCGTGATGTGTACGAAGCGCCCTTTTCGT 1164
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
|
Db 1165 CAGAACACACATGTTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA 1224
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
|
Db 1225 CTGTTATACTTACCAGTGCAGGGCGCTGAGACTTATGAAATGCTGTGTTGAAGATCAAAAG 1284
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
|
Db 1285 TCCCTGGAACCTCATGCACTACCTTCTCAGCACACAATTTGAAACGTACAGGCAACAGCAA 1344
```



```
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-590-64

Alignment Scores:
Pred. No.:      1,21e-276      Length:      2816
Score:          2383.00      Matches:      448
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              16          Gaps:          0

US-09-670-568C-1 (1-448) x US-10-393-590-64 (1-2816)

Qy      1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db      145 ATGTCCTCCAGAGCACACAGCAAAATGAATTCCTCAGTCAGAGGTTTCCAGCATATCTGG 204

Qy      21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db      205 GATTTTCTGGAAACAGCCTATATGTTTCAGTTCAGGCCCATTTGACTTGAACCTTTGTGGATGAA 264

Qy      41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetCln 60
Db      265 CCATCAGAAGATGGTGGCAACAAAGATTGAGATTAGCATGGACTGTATCCGATGCGAG 324

Qy      61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db      325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGCAACCTGGGGCTCTCTGACAGC 384

Qy      81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db      385 ATGGACACGACAGATTCAAGACGGCTCTCTGCTCCACAGTCCCTATTAACACAGACCAAGCG 444

Qy      101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db      445 CAGAACACGCTCAGCGGGCCCTCGCCCTACGACAGCCCGCAGCTCCACCTTCGATGCTCTC 504

Qy      121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db      505 TCTTCATCACCGGCATCCCTTCAACACCGACTACCCAGCGCCGCGCAGATTTCGACGTG 564

Qy      141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db      565 TCCTTCAGCAGCTCGAGCAGCCGCAAGTCGGCCACCTGGAGCGTATTCACCTGAACCTGAAG 624

Qy      161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db      625 AAATCTACTCCCAATTCGAAGACATGCCCCATCCAGATCAAGGGTATGACCCCACT 684

Qy      181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db      685 CCTCAGGAGCTGTATTCGGGCCATGCTCTCTACAAAAAAGCTGACGACGTCAAGGAG 744

Qy      201 ValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db      745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCGGTGAATTAACAGGGGACAGATTGCC 804

Qy      221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db      805 CCTCCTAGTCTATTTGATTTCGAGTAGAGGGGAACAGCCATGCCCATGTATGTAGAAGATCCC 864

Qy      241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
Db      865 ATCAGGAAGACAGAGTGTCTGTACCTTATGAGCCACCCAGGTGGACCTGAATTC 924

Qy      261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArg 280
Db      925 ACGACAGCTCTGTACAAATTTTCATGTAAACAGCAGCTTGTGTGGAGGATGAACCCCGCT 984

Qy      281 ProfileLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db      985 CCAATTTTAAATCATTTGTTACTCTCGAAACCCAGAGATGGCAAGTCTCTGGCGGACGCTGC 1044

Qy      301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db      1045 TTTGAGGCCCGGATCTGTCTTCCAGGAAGACAGAGGAGCGGATGAAGATAGCATC 1104

Qy      321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db      1105 AGAAAGCAGCAAGTTTCGACAGTACAAAGAACCGTATGTTACGAAGCGCCGCTTTCGT 1164

Qy      341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db      1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAAGATCCCCAGATGATGAA 1224

Qy      361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db      1225 CTGTTATACTTACCAGTGAAGGGCGGTGAGACTTATGAAATGCTGTTGAAGATCAAGAG 1284

Qy      381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db      1285 TCCCTGGAATCTATGCACTACCTTCTCAGCACAAATTGAAACGTACAGGCAACAGCAA 1344

Qy      401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuSerAlaCysPheArgAsnGlu 420
Db      1345 CAGCAGGACGACCCAGCACTTACTTCAGAAACATCTCTTTTCAGGCTGCTTCAGGAAATGAG 1404

Qy      421 LeuValGluProArgArgGluThrProLysGlnSerAspValPheArgHisSerLys 440
Db      1405 CTTGTGGAGCCCGGAGAGAAACTCCAAACAAATCTGACGCTCTCTTTAGACATTTCCAAG 1464

Qy      441 ProProAsnArgSerValTyrPro 448
Db      1465 CCCCCAACCCGATCAGTGTACCCA 1488

RESULT 10
US-10-393-590-65
; Sequence 65, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-590-65

Alignment Scores:
Pred. No.:      1,21e-276      Length:      2816
Score:          2383.00      Matches:      448
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              16          Gaps:          0

US-09-670-568C-1 (1-448) x US-10-393-590-65 (1-2816)

Qy      1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db      145 ATGTCCTCCAGAGCACACAGCAAAATGAATTCCTCAGTCAGAGGTTTCCAGCATATCTGG 204

Qy      21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db      925 ACGACAGCTCTGTACAAATTTTCATGTAAACAGCAGCTTGTGTGGAGGATGAACCCCGCT 984

Qy      261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArg 40
Db      985 CCAATTTTAAATCATTTGTTACTCTCGAAACCCAGAGATGGCAAGTCTCTGGCGGACGCTGC 1044
```

Db 205 GATTTCCTGGAAACAGCCTATATGTTTCAGTTCAGCCCATTTGACTTGAACATTTGTGGATGAA 264
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleAtrqMetGln 60
Db 265 CCATCAGAAGATGTTGGCAGCAACAAAGATTGAGATTAGCATGGATCTGTATCCGCATGCAG 324
Qy 61 AspSerAspLeuSerAspProMetTrrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATTTGCGCCACAGTACAGAACCTGGGGCTCCTGAAACAGC 384
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGGACACAGCAGATTCAAGACGGCTCTCGTCCACCATGTCCTATTAACACAGACCAGCG 444
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACAGCGTACCGCGCCCTCCCTTACGCACAGCCAGCTCCACTTCGATGCTCTC 504
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCGCCATCCCTCCCAACACCGACTACCCAGCGCCGCACAGTTTCGACGTG 564
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db 565 TCCTTCCAGCAGTCCAGCAGCGCCCAAGTCGGCCACCTGGACGTATTTCACCTGAACTGAAG 624
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACCTACTGCCAAATTGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCT 684
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CTTCAGGAGCTGTTATCCCGCCCATGCTCTACAAAAGCTGAGCAGCTCACCGAG 744
Qy 201 ValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGTCTGAGCGTGAATTTCAACAGGAGGACAGATTGCC 804
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CCTCCTAGTCTATTGATTCCAGTAGAGGGGAACAGCCATGCCCATGTAGTAGAGATCCC 864
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCACAGAAACAGAGATGCTGCTGTACCTTATGAGCCACCCAGCGTTGGCACTGAATTC 924
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACACACGTCTTGTACAAATTTTCATGTGTAAACAGCAGTTTGTGTGGAGGGATGAACCCCGT 984
Qy 281 ProfileLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgAtqCys 300
Db 985 CCAATTTTATCATTTACTCTCGAAACACAGATGGGCAAGTCTTGGGCGGACGCTGC 1044
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCCGGATCTGCTGTGCTCCAGGAAGACAGAGGAGCGGATGAAGATAGCATC 1104
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGACAGTACAAAGAACCGGTGATGGTACGAAGCGCCCGTTTCGT 1164
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGATATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA 1224
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1225 CTGTTACTTACAGTGAGGGGCGGTGAGACTTATGAATGCTGTGTTGAAGATCAAGAG 1284
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400

Db 1285 TCCTCGAACTCATGTCAGTACCTTCTCTCAGCACACAAATTGAAACGTATACAGGCAACAGAA 1344
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CACGACGACACCCAGCAGCTTACTTCAGAAACATCTCTTTTTCAGCCTGCTTCAGGAATGAG 1404
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1405 CTTGTGGAGCCCGGAGAGAACTCCAAACAAATCTGACGTCTTCTTTAGACATTCCCAAG 1464
Qy 441 ProProAsnArgSerValTyrPro 448
Db 1465 CCCCCAACCGATCAGTGTACCCA 1488
RESULT 11
US-10-393-567-26
; Sequence 26, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-567-26
Alignment Scores:
Pred. No.: 1,21e-276 Length: 2816
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-670-568C-1 (1-448) x US-10-393-567-26 (1-2816)
Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db 145 ATGTCCTCCAGACACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG 204
Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGAAACAGCCTATATGTTTCAGTTTCAGCCCATTTGACTTGAACCTTTGTGGATGAA 264
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleAtrqMetGln 60
Db 265 CCATCAGAAGATGTTGGCAGCAACAAAGATTGAGATTAGCATGGATGATTCGCGATGCAG 324
Qy 61 AspSerAspLeuSerAspProMetTrrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTCGCCACAGTACACAGAACCTGGGGCTCCTGAAACAGC 384
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGGACACAGCAGATTCAAGACGGCTCTCGTCCACCATGTCCTATTAACACAGACCAGCG 444
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACAGCGTACCGCGCCCTCCCTTACGCACAGCCAGCTCCACTTCGATGCTCTC 504
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCCCGCATCCCTCCCAACACCGACTACCCAGCGCCGCACAGTTTCGACGTG 564
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160

```
Db 565 TCCTCCAGCAGCTCGAGCACCAGCCAGTCGGCCACCTGGACGTATTCACCTGACCTGAAG 624
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAATCTACTGCCAAATTCGAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTATCCGGCCCATGCTGTCTACAAAAGAGCTGACGATCAGCGAG 744
Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCGGTGAATTCACAGGGGACAGATTGCC 804
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CCTCCTAGTCATTTGATTCSAGTAGAGGGGAACAGCCATGCCCATGTATGTAGAAGATCCC 864
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCAGAGGAACAGAGTGTCTGGTACTTATGAGCCACCCAGGTTGGCACTGAATTC 924
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArg 280
Db 925 ACGACAGTCTTGTACAATTTTCATGTGTAAACAGCAGTTGTGTGGAGGATGAACCGCGT 984
Qy 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgCys 300
Db 985 CCAATTTTAAATCATTTGTACTCTGGAAACACAGAGATGGGCAAGTCTGGGGCGACGTGC 1044
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCCGGATCTGTGCTTGTCCAGGAAGACAGAGAGCGGATGAAGATAGCATC 1104
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGATGTGTACGAAGCGCCGTTTCGT 1164
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGTATCCAGATGACATCCATCAAGAAACCAAGATCCCCAGATGATGAA 1224
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1225 CTGTATCTTACCAGTGAGGGCGGTGAGACTTATGAATGCTGTGAAGATCAAAAG 1284
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCCTGGAACCTCATGCACTACCTTCCTCAGCACACAATTTGAACGTACAGGCAACAGCAA 1344
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACATCTCCTTTTCAGCGCTGTTTCAGGAATGAG 1404
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1405 CTTGTGAGCCCCGGAGAGAAACTCCAAAACAATCTGACGCTCTCTTAGACATTCCTCAAG 1464
Qy 441 ProProAsnArgSerValTyrPro 448
Db 1465 CCCCCAAACCGATCAGTGTACCCA 1488
```

RESULT 12

```
US-10-393-567-27
; Sequence 27, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
```

```
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-567-27
```

Alignment Scores:

```
Pred. No.: 1,21e-276 Length: 2816
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
```

US-09-670-568C-1 (1-448) x US-10-393-567-27 (1-2816)

```
Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db 145 ATGTCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCCAGCATATCTGG 204
Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTCTGGAACAGCCTATATGTTTCAGTTTCAGCCCATTCGACTTGAACCTTTGTGATGAA 264
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 265 CCATCAGAAAGATGTCGCAACAAAGATTGAGATTAGCATGGAGCTGTATCCGCATGTCAG 324
Qy 61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACTCTGGGGCTCTCTGAACAGC 384
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGGACACGAGATTTCAGAACGGCTCTCTGTCACACAGTCCCTATATAACACAGACACCGG 444
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACAGCGCTCAGCGCGCCTCGCCCTACGCACAGCCAGCTCCACCTCGATGCTCTC 504
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCCGCCATCCCTCCACACACAGCTACCCAGCGCCGACAGTTTCGACGTG 564
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db 565 TCCTTCAGCAGTTCGAGCACCAGCCAGTCGCGCCACCTGGAGCTATTCCACTGAACCTGAG 624
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAATCTACTGCCAAATTCGAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCT 684
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTATTCGCGCCATGCTGTCTACAAAAGAGCTGAGCAGCTCAGCGAG 744
Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCGGTGAATTCACAGGGGACAGATTGCC 804
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CCTCCTAGTCATTTGATTTCAGTAGAGGGGAACAGCCATGCCCATGTATGTAGAAGATCCC 864
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCAGAGGAACAGAGATGTGCTGGTACTTATGAGCCACCCAGGTTGGCACTGAATTC 924
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArg 280
```

Db 925 ACACAGCTCTGTACAAATTTTCATGTGAACAGCAGTGTGTGTGGAGGATGAACCGCGT 984
Qy 281 ProfileLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgCys 300
Db 985 CCAATTTTAAATCATGTGTACTCTGGAACACAGAGATGGGCAAGTCTTGGGCCGACGCTGC 1044
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCCGGATCTGTCTTGGCCAGGAAGACAGAGGAGCGGATGAAGATAGCATC 1104
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACCGTGTATGTCAGAAAGCGCCGTTTCGT 1164
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGTATCCAGATGACATCCATCAAGAAACGAAGATCCCGAGATGATGAA 1224
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysLysGlu 380
Db 1225 CTGTATACCTACCAAGTGGGGCCGTGAGACTTATGAATGCTGTGTGAAGATCAAGAG 1284
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCTTGGAACTCATGCACTACCTTCTCAGCACACAATTGAAACGTCACAGGCAACAGCAA 1344
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCAGCAGCAGCACTTACTTCAGAAACATCTCCTTCAGCCGCTTCAGGAATGAG 1404
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1405 CTTGTGGAGCCCCGGAGAGAACTCCAAACAATCTGACGCTCTTCCTTAGACATTCGAAG 1464
Qy 441 ProProAsnArgSerValTyrPro 448
Db 1465 CCCCCAACCGATCAGTGTATCCCA 1488

RESULT 13

US-10-393-567-64

; Sequence 64, Application US/10393567

; Publication No. US20030194733A1

; GENERAL INFORMATION:

; APPLICANT: WANG, YIXIN

; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL

; FILE REFERENCE: CDS 269 US NP

; CURRENT APPLICATION NUMBER: US/10/393,567

; CURRENT FILING DATE: 2003-03-21

; PRIOR APPLICATION NUMBER: 60/368,667

; PRIOR FILING DATE: 2002-03-29

; NUMBER OF SEQ ID NOS: 100

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 64

; LENGTH: 2816

; TYPE: DNA

; ORGANISM: human

US-10-393-567-64

Alignment Scores:

Pred. No.:	1,21e-276	Length:	2816
Score:	2383.00	Matches:	448
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	16	Gaps:	0

US-09-670-568c-1 (1-448) x US-10-393-567-64 (1-2816)

Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTyr 20

Db 145 ATGTCCAGAGCACACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCAGCATATCTGG 204

Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGACAGCGCTATATGTTTCAGTTCAGCCCATTTGACATTGTTGTTGGATGAA 264
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 265 CCATCAGAAGATGGTGCAGACAAACAAGATTGAGATTGACATGGACATGTATCCGCATGCAG 324
Qy 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACGAACTCTGGGGCTCTCTGAACAGC 384
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGGACACAGATTTCAGAACCGCTCTCGTCCACCACTCCCTATTAACACAGACCAACGCG 444
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACAGCGCTCAGCGCGCCCTCGCCCTACGCACAGCCAGCTCCACCTTCGATGCTCTC 504
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATACCCCGCCATCCCTCCAAACACCGACTACCCAGGCCCGCACAGTTTCGAGCTG 564
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
Db 565 TCCTTCCAGCAGTCGAGCACCGCCCAAGTCGGCCACCTGGACGCTATTTCCTCACTGAAC 624
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACCTCTACTGCCAAATTGCAAGACATGCCCCATCCAGATCAAGGTGATGACCCCACT 684
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CTCAGGAGCTGTTATCCGGCCATGCTCTGTCTACAAAAAAGCTCAGGCACGTCACGGAG 744
Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCAAACAGGAGCAGATTGCC 804
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CTTCTCTAGTCATTTGATTTCGAGTAGAGGGGAACAGCCATGCCCAGTATGTAGAAGATCCC 864
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCAGAGGAAGACAGAGTGTGTGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 924
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACGACAGTCTTGTACAAATTTTCATGTGTAACAGCAGTGTGTGTGGAGGGATGAACCCCGT 984
Qy 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 985 CCAATTTTAAATCATTTACTCTCGAAACACAGAGATGGGCAAGTCTCTGGGCCCGCGCTGC 1044
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCCGGATCTGTCTTGGCCAGGAAGACAGAGGCGGATGAAGATGATCATC 1104
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAAGCAGCAAGTTTTCGGACAGTACAAAGAACCGTGTATGTAAGAGCCGCCGCTTCGT 1164
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCGCATATGATGAA 1224
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysLysGlu 380
Db 1225 CTGTATACCTACCAAGTGGGGCCGCTGAGACTTATGAATGCTGTGTGAAGATCAAGAG 1284
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400

; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/369,790
; FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-394-087-26

Alignment Scores:
Pred. No.: 1,21e-276 Length: 2816
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-670-568C-1 (1-448) x US-10-394-087-26 (1-2816)

```
Qy      1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTyr 20
Db      145 ATGTCACAGAGCACACAGAAATGAAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG 204

Qy      21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db      205 GATTTCTCGAAGACGCTATATGTTCACTTCAGGCCCATTCAGTTGAACTTTGTGGATGAA 264

Qy      41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db      265 CCATCAGAAGATGTGGCAGACAAACAGATTGAGATTAGCATGGAGCTGTATCCGCATCGAG 324

Qy      61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db      325 GACTCGGACCTTGAGTGACCCCATGTGGCCACAGTACAGAACCTTGGGGCTCTCTGAACAGC 384

Qy      81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db      385 ATGGACACGACAGATTGAGAACGGCTCTCTGCTCCACCATGCTCCATTAACACAGACACCGC 444

Qy      101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db      445 CAGAACACGCTCAGCGGGCCCTCGCCCTTACGACAGACCCAGCTCCAGCTTCGATGCTCTC 504

Qy      121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db      505 TCTCCATCACCCGCGCATCCCTCCAAACACCGACCTACCCAGGCCCGCCACAGTTTCGACGTG 564

Qy      141 SerPheGlnGlnSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db      565 TCCTTCCAGCAGTCGAGCACCGCCCAAGTCGCGCCACCTGGAGGTATTCACCTGAACCTGAAG 624

Qy      161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db      625 AAACCTACTGCCAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684

Qy      181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db      685 CCTCAGGAGGCTGTATTCGCGGCATGCTGTCTACAAAAAAGCTGAGCAGCTCAGCGAG 744

Qy      201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db      745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCACAGGGGACAGATTGCC 804

Qy      221 ProProSerHisLeuIleArgValIleGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db      805 CCTCCTAGTCATTTGATTGAGTAGAGGGGAACAGCCATGCCCCAGTATGTAGAAGATCCC 864

Qy      241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db      865 ATCAGGAAGACAGAGTGTGTGTACCTTATGAGCCACCCAGGTGGCACCTGAATTC 924
```

```
Qy      261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db      925 ACCACAGTCTTTGTACAATTTTCATGTGTAAACAGCAGTGTGTGGAGGGATGAACCGCGT 984

Qy      281 ProIleIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db      985 CCAATTTTAAATCATTTGTACTCTGGAAACACAGAGATGGGCAAGTCTTGGGCCGACGCTGC 1044

Qy      301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db      1045 TTTGAGGCCCGGATCTGTCTTCCCCAGGAAGACAGAGGAGCGGATGAAGATAGCATC 1104

Qy      321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db      1105 AGAAAGCAGCAAGTTTTCGGACAGTACAAAGAACGGTATGGTACGAAGCCCGCTTTTCGT 1164

Qy      341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db      1165 CAGAACACATGGTATCCAGATGATCCATCCAGAAACGAAGATCCCCAGATGATGAA 1224

Qy      361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db      1225 CTGTTATCTTACTTACAGTGAGGGSCCGTGAGACTTATGAAATGCTGTTGAAGATCAAGAG 1284

Qy      381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db      1285 TCCCTGGAACCTCATGCACTACCTTCTCTCAGCACACAATTTGAAACGTCACAGGCAACGCAA 1344

Qy      401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db      1345 CAGCAGCAGCACCCAGCACCTTACTTTCAGAAACATCTCTCTTTCAGCCTGCTTCAGGAATGAG 1404

Qy      421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db      1405 CTTGTGGAGCCCGGAGAGAAACTCCAAAAACAATCTGACGCTCTCTTTAGACATTTCCAAG 1464

Qy      441 ProProAsnArgSerValTyrPro 448
Db      1465 CCCCCAACCGATCAGTGTACCCA 1488
```

Search completed: October 3, 2005, 06:22:31
Job time : 971 secs

Query Match 100.0%; Score 2816; DB 9; Length 2816; Best Local Similarity 100.0%; Pred. No. 0; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	TCGTTGATATCAAGACAGTTGAAGGAATGAATTTTGAACCTTCACGGTGTGCCACCT	60						
DB	1	TCGTTGATATCAAGACAGTTGAAGGAATGAATTTTGAACCTTCACGGTGTGCCACCT	60						
QY	61	ACAGTACTGCCCTGACCTTACATTCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG	120						
DB	61	ACAGTACTGCCCTGACCTTACATTCAGCGTTTCGTAGAACCCAGCTCATTTCTCTGG	120						
QY	121	AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGACAAATGAATTCCTCAGT	180						
DB	121	AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGACAAATGAATTCCTCAGT	180						
QY	181	CGAGAGTTTCCAGCATATCTGGATTTCTGGAACAGCCATATGTTTCAGTTCAGCCC	240						
DB	181	CGAGAGTTTTCAGCATATCTGGATTTCTGGAACAGCCATATGTTTCAGTTCAGCCC	240						
QY	241	ATTGACTTGAACCTTTGTGGATGAACCATCAGAAAGATGGTCGACAAACAAAGATTGAGATT	300						
DB	241	ATTGACTTGAACCTTTGTGGATGAACCATCAGAAAGATGGTCGACAAACAAAGATTGAGATT	300						
QY	301	AGCATGGACTGTATCCGCATGCGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC	360						
DB	301	AGCATGGACTGTATCCGCATGCGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC	360						
QY	361	ACGAACCTGGGCTCTGAAACAGATGGACCCAGCATTCAGAACCGCTCTCGTCCACC	420						
DB	361	ACGAACCTGGGCTCTGAAACAGATGGACCCAGCATTCAGAACCGCTCTCGTCCACC	420						
QY	421	AGTCCCTATTAACACAGACACGGCGAGAACAGCGTCAAGCGGCTCGCCCTACGCACAG	480						
DB	421	AGTCCCTATTAACACAGACACGGCGAGAACAGCGTCAAGCGGCTCGCCCTACGCACAG	480						
QY	481	CCAGCTCCACCTTCGATGCTCTCTCCATCACCCGCCATCCCTCCAAACCCGACTAC	540						
DB	481	CCAGCTCCACCTTCGATGCTCTCTCCATCACCCGCCATCCCTCCAAACCCGACTAC	540						
QY	541	CCAGGCCCCGACAGTTTCCAGCTGCTCTCCAGCAGTCGAGCACCCGCAAGTCGGCCACC	600						
DB	541	CCAGGCCCCGACAGTTTCCAGCTGCTCTCCAGCAGTCGAGCACCCGCAAGTCGGCCACC	600						
QY	601	TGGACCTATTCCACTGAAGAACTCTACTGCGCAAAATTCGAAAGACATGCCCCATC	660						
DB	601	TGGACCTATTCCACTGAAGAACTCTACTGCGCAAAATTCGAAAGACATGCCCCATC	660						
QY	661	CAGATCAAGGTGATGATACCCCACTCTCAGGGAGCTGTTATCCGCCCATGCTGTCTAC	720						
DB	661	CAGATCAAGGTGATGATACCCCACTCTCAGGGAGCTGTTATCCGCCCATGCTGTCTAC	720						
QY	721	AAAAAGCTGAGCAGCTCAGGAGTGGTGAGCGGTGCCCAACCATGAGCTGAGCCGT	780						
DB	721	AAAAAGCTGAGCAGCTCAGGAGTGGTGAGCGGTGCCCAACCATGAGCTGAGCCGT	780						
QY	781	GAATTCAAACGAGGACAGATTGCCCTCTCTAGTCAATTTGATTTCGAGTAGGGGAACAGC	840						
DB	781	GAATTCAAACGAGGACAGATTGCCCTCTCTAGTCAATTTGATTTCGAGTAGGGGAACAGC	840						
QY	841	CATGCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGTGTAACCTTAAGAG	900						
DB	841	CATGCCAGTATGTAGAAGATCCCATCACAGGAAGACAGAGTGTGTGTAACCTTAAGAG	900						
QY	901	CCACCCAGGTTGGCACTGAATTCAGCAGCTCTGTACAATTTCAATTCATGTGTACACAGCT	960						
DB	901	CCACCCAGGTTGGCACTGAATTCAGCAGCTCTGTACAATTTCAATTCATGTGTACACAGCT	960						
QY	961	TGTGTTGGAGGGATGAACCGCGCTCCAAATTTTAAATCAATTTTACTCTGGAACACAGAT	1020						
DB	961	TGTGTTGGAGGGATGAACCGCGCTCCAAATTTTAAATCAATTTTACTCTGGAACACAGAT	1020						
QY	1021	GGGCAAGTCTCTGGGCGGACGCTGCTTTTGAGGCCCGGATCTGTGCTTGGCCAGGAGAGAC	1080						

DB	1021	GGGCAAGTCTCTGGGCGGACGCTGCTTTGAGGCCCGGATCTGTGCTTGGCCAGGAGAC	1080						
QY	1081	AGGAAGGGGATGAAGATAGCATCAGAAAGCAGCAGTAAGTTTCGGACAGTACAAGACGGT	1140						
DB	1081	AGGAAGGGGATGAAGATAGCATCAGAAAGCAGCAGTAAGTTTCGGACAGTACAAGACGGT	1140						
QY	1141	GATGCTACGAAGCGCCGTTTCGTGAGAACACACATGTTATCCAGATGACATCCATCAAG	1200						
DB	1141	GATGCTACGAAGCGCCGTTTCGTGAGAACACACATGTTATCCAGATGACATCCATCAAG	1200						
QY	1201	AAACGAAGATCCCGAGATGAATGTTTATCTTACAGTGAGGGCGCGTGAGACTTAT	1260						
DB	1201	AAACGAAGATCCCGAGATGAATGTTTATCTTACCAGTGAGGGCGCGTGAGACTTAT	1260						
QY	1261	GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGSCAGTACTCTTCTCAGCACACA	1320						
DB	1261	GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGSCAGTACTCTTCTCAGCACACA	1320						
QY	1321	ATTGAAACGTTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1380						
DB	1321	ATTGAAACGTTACAGGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	1380						
QY	1381	CTTTGAGCCTGCTTCAGGAATGAGCTTGTGAGAGCCCGGAGAGAGAACTCCAAAACATCT	1440						
DB	1381	CTTTGAGCCTGCTTCAGGAATGAGCTTGTGAGAGCCCGGAGAGAGAACTCCAAAACATCT	1440						
QY	1441	GACGCTCTCTTTAGACATTCGAAAGCCCAACCCAGTCACTGCTACCCATAGAGCCCTATC	1500						
DB	1441	GACGCTCTCTTTAGACATTCGAAAGCCCAACCCAGTCACTGCTACCCATAGAGCCCTATC	1500						
QY	1501	TCATATTTTAAAGTGTGTGTGTTTATTTCCATGTATATGTGATGTGTGTGTGTGTA	1560						
DB	1501	TCATATTTTAAAGTGTGTGTGTTTATTTCCATGTATATGTGATGTGTGTGTGTGTA	1560						
QY	1561	TGTGTGTGTGTGTGTATCTAGCCCTCATAAACAGACATTTGAAGACACTTTGGCTCAGAGA	1620						
DB	1561	TGTGTGTGTGTGTATCTAGCCCTCATAAACAGACATTTGAAGACACTTTGGCTCAGAGA	1620						
QY	1621	CCCAACTGCTCAAGGCAACAAAGCCACTAGTCAGAGAACTCTTTTGAAGGAGCTCAAACT	1680						
DB	1621	CCCAACTGCTCAAGGCAACAAAGCCACTAGTCAGAGAACTCTTTTGAAGGAGCTCAAACT	1680						
QY	1681	TTACAAGAAAGGATGTTTCTGACAGATTTGTATCTTTAGACCCGCGCATTTGGTGGTGAG	1740						
DB	1681	TTACAAGAAAGGATGTTTCTGACAGATTTGTATCTTTAGACCCGCGCATTTGGTGGTGAG	1740						
QY	1741	GAAACACTGT	1800						
DB	1741	GAAACACTGT	1800						
QY	1801	GAAAGGGGCTTAAAGATGTTTATTTGAAACCCCTTTTCTGTCTCTCTGTGTGTGTGTGTAA	1860						
DB	1801	GAAAGGGGCTTAAAGATGTTTATTTGAAACCCCTTTTCTGTCTCTCTGTGTGTGTGTGTAA	1860						
QY	1861	AATTCAAGGGGAGCTTTTGAAGAGCTCTCAAACTTAAAGATGCTTTTTTAAGAAAAGGAG	1920						
DB	1861	AATTCAAGGGGAGCTTTTGAAGAGCTCTCAAACTTAAAGATGCTTTTTTAAGAAAAGGAG	1920						
QY	1921	AAAAAGTTGTTTGTCTGTGCATTAAGTNAAGTTCTAGTGTAGTGTAGTGTAGTGTAGTGT	1980						
DB	1921	AAAAAGTTGTTTGTCTGTGCATTAAGTNAAGTTCTAGTGTAGTGTAGTGTAGTGTAGTGT	1980						
QY	1981	CCCTTTTAAATGCTGT	2040						
DB	1981	CCCTTTTAAATGCTGT	2040						
QY	2041	TACTGCTGGGAGCGAGGTGATCATTAACAAAGTAATCAACTTTGTGGGTGGAGAGTTC	2100						
DB	2041	TACTGCTGGGAGCGAGGTGATCATTAACAAAGTAATCAACTTTGTGGGTGGAGAGTTC	2100						
QY	2101	TTTGTGAGAACTTGATTTTGT	2160						

```
Db 2101 TTGTGGAAGACTTGCAATTAATTTGTGCTCTCCCTCATGTAGGTAGAACATTTCTTAAT 2160
Qy GCTGTGACCTGCTCTGCCACTGTATGCTTGGCATCTGTTATGCTTAAAGTTTTTCTTGTA 2220
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2220
Qy GCTGTGACCTGCTCTGCCACTGTATGCTTGGCATCTGTTATGCTTAAAGTTTTTCTTGTA 2280
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2280
Qy CATGAACCCCTGGAGACCTACTACAAAGAACTGTTGTTGGCCCCCATAGCAGGTGAA 2340
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2340
Qy CTGATTTTGTCTTTTAATAGAAAGCAAAATCCACCCAGTAATATTGCCCCCTTACGTAGT 2400
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2400
Qy TGTTTACCAATTAACAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAATACTCTGTATT 2460
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2460
Qy TGTTTACCAATTAACAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAATACTCTGTATT 2520
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2520
Qy AAATTTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCTACATAAAACCCAGCCATATTA 2580
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2580
Qy AAATTTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACCTACATAAAACCCAGCCATATTA 2640
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2640
Qy CTGATACCTGTCAGTGAATTTAGCAAGAGACTTACGTTTGTAGTAAGTGAATCCAAAGC 2700
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2700
Qy CTGATACCTGTCAGTGAATTTAGCAAGAGACTTACGTTTGTAGTAAGTGAATCCAAAGC 2760
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2760
Qy AGAGCTGTTAAATCAGCACTCTGGACTGGAAATTAAGATTTGAAAGGTTAGACTACTT 2816
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2816
Qy AGAGCTGTTAAATCAGCACTCTGGACTGGAAATTAAGATTTGAAAGGTTAGACTACTT 2880
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2880
Qy TTCTTTTTTACTCAAAAGTTTGAAGAACTCTGTTTCTTCTTCCATTTTAAACATATT 2940
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2940
Qy TTCTTTTTTACTCAAAAGTTTGAAGAACTCTGTTTCTTCTTCCATTTTAAACATATT 3000
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3000
Qy TTAAGATAATAGCAATAAGACTTTTAAAGTTTCTCTCCCTCCATCTTCCACACCCAGT 3060
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3060
Qy TTAAGATAATAGCAATAAGACTTTTAAAGTTTCTCTCCCTCCATCTTCCACACCCAGT 3120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3120
Qy CACCAGCACTGTATTTCTGTGCACCAAGCAATGATTTCTGTTATTGAGGCTGTGCTT 3180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3180
Qy CACCAGCACTGTATTTCTGTGCACCAAGCAATGATTTCTGTTATTGAGGCTGTGCTT 3240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 3240
Qy TTGTGGATGTGATTTTAAATTTCAATAAACTTTTGCACTTGTGTTTAAAGAAA 2816
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2816
Qy TTGTGGATGTGATTTTAAATTTCAATAAACTTTTGCACTTGTGTTTAAAGAAA 2880
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 2880

RESULT 2
US-09-850-716A-333
; Sequence 333, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-850-716A-333

Query Match 100.0%; Score 2816; DB 9; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCGTTGATATCAAGACAGTTGAAGAAATGAATTTTGAACCTTCAAGTGTGCCACCT 60
```

```
Db 1 TCGTTGATATCAAGACAGTTGAAGAAATGAATTTTGAACCTTCAAGTGTGCCACCT 60
Qy ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTTTGG 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 120
Qy ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTTTGG 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 180
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 240
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 300
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 360
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 420
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 420
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 480
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 480
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 540
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 540
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 600
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 600
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 660
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 660
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 720
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 720
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 780
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 780
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 840
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 840
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 900
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 900
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 960
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 960
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 1020
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 1020
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 1080
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 1080
Qy AAAGAAAGTTTATTACCGATCCAGCATGCCAGAGCACAGACAAATGAATTTCTCAGT 1140
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 1140
```


QY 1 TCGTTGATATCAAGACAGTGTGAAGAAATGAATTTTGAACCTTCAACGGTGTGCCACCT 60
DB 1 TCGTTGATATCAAGACAGTGTGAAGAAATGAATTTTGAACCTTCAACGGTGTGCCACCT 60
QY 61 ACAGTACTGCGCTGACCCCTTACATCCAGGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
DB 61 ACAGTACTGCGCTGACCCCTTACATCCAGGTTTCGTAGAAACCCAGCTCATTTCTCTTGG 120
QY 121 AAAGAAAGTTATTTACCGATCCACCATGTCCAGAGACACACAGACAAATGAATTTCTCAGT 180
DB 121 AAAGAAAGTTATTTACCGATCCACCATGTCCAGAGACACACAGACAAATGAATTTCTCAGT 180
QY 181 CCAGAGTTTCCAGCATATCTGGGATTTTCTGGAAACAGCCTATATGTTTCAAGTTCAAGCCC 240
DB 181 CCAGAGTTTCCAGCATATCTGGGATTTTCTGGAAACAGCCTATATGTTTCAAGTTTCAAGCCC 240
QY 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAGATGGTGGACAAACAAGATTGAGATT 300
DB 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAGATGGTGGACAAACAAGATTGAGATT 300
QY 301 AGCATGGAATGTATCCGATCCAGACTTCGGACCTGAGTGACCCCATGTGGCCACAGTAC 360
DB 301 AGCATGGAATGTATCCGATCCAGACTTCGGACCTGAGTGACCCCATGTGGCCACAGTAC 360
QY 361 ACGAACCTTGGGCTCTCTGAAACAGATGGAACAGAGATTCAGAACGGCTCTCTGCTCCACC 420
DB 361 ACGAACCTTGGGCTCTCTGAAACAGATGGAACAGAGATTCAGAACGGCTCTCTGCTCCACC 420
QY 421 AGTCCCTATACACAGACCCGACAGCTCAGGCGCTCAGGCGCTCGCCCTAGCCACAG 480
DB 421 AGTCCCTATACACAGACCCGACAGCTCAGGCGCTCAGGCGCTCGCCCTAGCCACAG 480
QY 481 CCCAGCTCCACCTTTCGATGCTCTCTCCATCACCCTGCTCCCAACCCGACTAC 540
DB 481 CCCAGCTCCACCTTTCGATGCTCTCTCCATCACCCTGCTCCCAACCCGACTAC 540
QY 541 CCAGGCCGACAGTTTCGAGTGTCTTCCAGAGTGGAGCAACGGCAAGTGGGCCACC 600
DB 541 CCAGGCCGACAGTTTCGAGTGTCTTCCAGAGTGGAGCAACGGCAAGTGGGCCACC 600
QY 601 TGGACGTATTCACCTGAACAACTCTACTGCCAATTTGCAAGACATGCCCATC 660
DB 601 TGGACGTATTCACCTGAACAACTCTACTGCCAATTTGCAAGACATGCCCATC 660
QY 661 CAGATCAAGGTGATGACCCACCTCTCAGGAGCTGTATCCGCGCATGCCCTGTCTAC 720
DB 661 CAGATCAAGGTGATGACCCACCTCTCAGGAGCTGTATCCGCGCATGCCCTGTCTAC 720
QY 721 AAAAAAGCTGACGACGTGAGCGGTGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
DB 721 AAAAAAGCTGACGACGTGAGCGGTGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
QY 781 GAATTCACAGGGACAGATTGCCCTCCTAGTCAATTTGATTCAGTAGAGGGGAAACAGC 840
DB 781 GAATTCACAGGGACAGATTGCCCTCCTAGTCAATTTGATTCAGTAGAGGGGAAACAGC 840
QY 841 CATGCCAGTATGTAGAAGATCCCATCACAGGAACAGAGTGTGCTGCTACCTTATGAG 900
DB 841 CATGCCAGTATGTAGAAGATCCCATCACAGGAACAGAGTGTGCTGCTACCTTATGAG 900
QY 901 CCACCCAGGTGTGCACTGAATTCACGACAGTCTTGTACAAATTTTCAATGTGTAAACAGAGT 960
DB 901 CCACCCAGGTGTGCACTGAATTCACGACAGTCTTGTACAAATTTTCAATGTGTAAACAGAGT 960
QY 961 TGTGTTGGAGGGATGAACCCGCTGCAATTTTAATCAATTTTACTCTGGAACACAGAGAT 1020
DB 961 TGTGTTGGAGGGATGAACCCGCTGCAATTTTAATCAATTTTACTCTGGAACACAGAGAT 1020
QY 1021 GGGCAAGTCTTGGCCGACGCTGCTTTGAGCCCGGATCTGTGCTCCCGCAGGAAGAGAC 1080
DB 1021 GGGCAAGTCTTGGCCGACGCTGCTTTGAGCCCGGATCTGTGCTCCCGCAGGAAGAGAC 1080
QY 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT 1140

DB 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGT 1140
QY 1141 GATGGTACGAAGCCGCGTTTCGTAGAAACACATGGTATCCAGATGACATCCATCAAG 1200
DB 1141 GATGGTACGAAGCCGCGTTTCGTAGAAACACATGGTATCCAGATGACATCCATCAAG 1200
QY 1201 AAACGAAGATCCCCAGATGATGAACCTGTATACCTTACCAGTGAGGGCCGTGAGACTTAT 1260
DB 1201 AAACGAAGATCCCCAGATGATGAACCTGTATACCTTACCAGTGAGGGCCGTGAGACTTAT 1260
QY 1261 GAAATGCTGTTGAAGATCAAAAGAGTCCCTGGAACCTCATGCAAGTACCTTCTCAGCACACA 1320
DB 1261 GAAATGCTGTTGAAGATCAAAAGAGTCCCTGGAACCTCATGCAAGTACCTTCTCAGCACACA 1320
QY 1321 ATTGAACAGTACAGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
DB 1321 ATTGAACAGTACAGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
QY 1381 CTTTCAGCCTGCTTTCAGGAATGAGCTTGTGAGCCCGGAGAGAAACCTCCAAACCAATCT 1440
DB 1381 CTTTCAGCCTGCTTTCAGGAATGAGCTTGTGAGCCCGGAGAGAAACCTCCAAACCAATCT 1440
QY 1441 GACGCTCTTTCAGCAATTCGAAGCCCCCAAAACCGATCAGTGATCCCATAGAGCCCTATC 1500
DB 1441 GACGCTCTTTCAGCAATTCGAAGCCCCCAAAACCGATCAGTGATCCCATAGAGCCCTATC 1500
QY 1501 TCTATATTTTAAAGTGTGTGTGTATTTCCATGTGTATATGTCAGTGTGTGTGTGTA 1560
DB 1501 TCTATATTTTAAAGTGTGTGTGTATTTCCATGTGTATATGTCAGTGTGTGTGTGTA 1560
QY 1561 TGTGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACATTTGGCTCAGAGA 1620
DB 1561 TGTGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACATTTGGCTCAGAGA 1620
QY 1621 CCNAACCTGCTCAAAGGCACAAAGCCACTAGTGAGAGAACTTTTGAAGGGAACCTCAAACCT 1680
DB 1621 CCNAACCTGCTCAAAGGCACAAAGCCACTAGTGAGAGAACTTTTGAAGGGAACCTCAAACCT 1680
QY 1681 TTAACAAGAAAGGATGTTTTCTGCGATTTTGTATCTTAGACCGGCACTTGGTGGGTGAG 1740
DB 1681 TTAACAAGAAAGGATGTTTTCTGCGATTTTGTATCTTAGACCGGCACTTGGTGGGTGAG 1740
QY 1741 GAACCACTGTGTTTTCTGTGAGCTTTCTGTGTTTCTCGGAGGAGGGGTGAGGTGGG 1800
DB 1741 GAACCACTGTGTTTTCTGTGAGCTTTCTGTGTTTCTCGGAGGAGGGGTGAGGTGGG 1800
QY 1801 GAAAGGGGCAATTAAGATGTTTATTTGGAACCCCTTTCTGTCTTCTGTTGTTTTCTAA 1860
DB 1801 GAAAGGGGCAATTAAGATGTTTATTTGGAACCCCTTTCTGTCTTCTGTTGTTTTCTAA 1860
QY 1861 AATTCACAGGGAAGCTTTTGAGCAGGTCCTCAAACTTAAGATGCTCTTTTAAGAAAGGAG 1920
DB 1861 AATTCACAGGGAAGCTTTTGAGCAGGTCCTCAAACTTAAGATGCTCTTTTAAGAAAGGAG 1920
QY 1921 AAAAAAGTTGTTATTTGTCTGATTAAGTAAGTTGTAGGTGACTGAGAGACTCAGTACAGA 1980
DB 1921 AAAAAAGTTGTTATTTGTCTGATTAAGTAAGTTGTAGGTGACTGAGAGACTCAGTACAGA 1980
QY 1981 CCCTTTTAAATGCTGCTCATGTAATAATTTGCAAGTAGTAAGAAACGAAGGTGTCAAGTG 2040
DB 1981 CCCTTTTAAATGCTGCTCATGTAATAATTTGCAAGTAGTAAGAAACGAAGGTGTCAAGTG 2040
QY 2041 TACTGCTGGCAGCGAGGTGATCATTTACCAAAAGTAAATCACTTTTGGGTGGAGAGTTC 2100
DB 2041 TACTGCTGGCAGCGAGGTGATCATTTACCAAAAGTAAATCACTTTTGGGTGGAGAGTTC 2100
QY 2101 TTTGTGAGAACTTTCGATTTATTTGTCTCCCTCATGTGTAGGTAGAAACATTTCTTAAT 2160
DB 2101 TTTGTGAGAACTTTCGATTTATTTGTCTCCCTCATGTGTAGGTAGAAACATTTCTTAAT 2160
QY 2161 GCTGTGTACTGCTCTGCGACCTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCTTGTA 2220

Db 2161 GCTGTGTACCTGCTCTGCGCACTGTATGTTGGCACTGTGTTATGCTAAAGTTTTTCTTGTA 2220
QY 2221 CATGAACCCCTGGAAGACCTTACTACAAAATACTGTTGTTGGCCCTCCATAGCAGTGAA 2280
Db 2221 CATGAACCCCTGGAAGACCTTACTACAAAATACTGTTGTTGGCCCTCCATAGCAGTGAA 2280
QY 2281 CTCATTTTGTGCTTTTAAATAGAAGACAAATCCACCCCACTAATATTGCCCTTACGTAGT 2340
Db 2281 CTCATTTTGTGCTTTTAAATAGAAGACAAATCCACCCCACTAATATTGCCCTTACGTAGT 2340
QY 2341 TGTTTACCATTATCAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATT 2400
Db 2341 TGTTTACCATTATCAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATT 2400
QY 2401 AATTTGCTTAAATAGAGCTTCTATCCTCAAGCTTACCTACCATAAAACCAGCCATATTA 2460
Db 2401 AATTTGCTTAAATAGAGCTTCTATCCTCAAGCTTACCTACCATAAAACCAGCCATATTA 2460
QY 2461 CTGATCTGTTCACTGATTTTACCCAGGAGACTTACGTTTGGTAAAGTGAGATCCAAGC 2520
Db 2461 CTGATCTGTTCACTGATTTTACCCAGGAGACTTACGTTTGGTAAAGTGAGATCCAAGC 2520
QY 2521 AGACGTGTTAAATACAGCACTCTCGACTGGAATTAAGATTTGAAGGGTAGACTACTT 2580
Db 2521 AGACGTGTTAAATACAGCACTCTCGACTGGAATTAAGATTTGAAGGGTAGACTACTT 2580
QY 2581 TTCTTTTCTTACTCAAAAGTTTAGAGAACTCTGTTTCTTCTTCCATTTTAAAAACATATT 2640
Db 2581 TTCTTTTCTTACTCAAAAGTTTAGAGAACTCTGTTTCTTCTTCCATTTTAAAAACATATT 2640
QY 2641 TTAAGATAATAGCATAAAGACTTTTAAATGTTTCTCCCTCCCTCCATCTTCCACACCCAGT 2700
Db 2641 TTAAGATAATAGCATAAAGACTTTTAAATGTTTCTCCCTCCCTCCATCTTCCACACCCAGT 2700
QY 2701 CACCAGCACTGATTTTCTGTCAAAAGCAATGATTTCTGTTATAGGCTGTGCTT 2760
Db 2701 CACCAGCACTGATTTTCTGTCAAAAGCAATGATTTCTGTTATAGGCTGTGCTT 2760
QY 2761 TTGTGATGTGATTTTAAATTTTAAATTTTCAATTAACCTTTTGCATCTTGGTTTAAAGAAA 2816
Db 2761 TTGTGATGTGATTTTAAATTTTAAATTTTCAATTAACCTTTTGCATCTTGGTTTAAAGAAA 2816

RESULT 4

US-10-007-700-333
; Sequence 333, Application US/10007700
; Publication No. US20030064947A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihito
; APPLICANT: Peckman, David W.
; APPLICANT: Cai, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C17
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 333

; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-700-333
Query Match 100.0%; Score 2816; DB 14; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTTGATATCAAGACAGTTCGAAGAAATGAATTTTGAACCTTCACGGTGTGCCACCT 60
Db 1 TCGTTGATATCAAGACAGTTCGAAGAAATGAATTTTGAACCTTCACGGTGTGCCACCT 60
QY 61 ACAGTACTGCCCTGACCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTGG 120
Db 61 ACAGTACTGCCCTGACCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTGG 120
QY 121 AAAGAAAGTTATACCGATCCACATGTCCTCCAGAGCAGACAGACAAATGAATTCCTCAGT 180
Db 121 AAAGAAAGTTATACCGATCCACATGTCCTCCAGAGCAGACAGACAAATGAATTCCTCAGT 180
QY 181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAAACAGCCTATATGTTTCAGTTCAGCCC 240
Db 181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGGAAACAGCCTATATGTTTCAGTTCAGCCC 240
QY 241 ATTGACTTTGAACTTTGTGGATGAACCATCAGAAAGATGTTGCGACAAACAAGATTGAGATT 300
Db 241 ATTGACTTTGAACTTTGTGGATGAACCATCAGAAAGATGTTGCGACAAACAAGATTGAGATT 300
QY 301 AGCATGGACTGATCCGATGTCAGGACCTGGAACCTTGAAGTGAACCCATGTTGGCCACAGTAC 360
Db 301 AGCATGGACTGATCCGATGTCAGGACCTGGAACCTTGAAGTGAACCCATGTTGGCCACAGTAC 360
QY 361 AGCAACCTGGGCTCTCTGAACAGCATGACACAGAGATTCAGAAACGGCTCTCGTCCACC 420
Db 361 AGCAACCTGGGCTCTCTGAACAGCATGACACAGAGATTCAGAAACGGCTCTCGTCCACC 420
QY 421 AGTCCCTATAACACAGACCAACCGCAGAACACGCGTCAACGGCCCTTCGCCCTACGCACAG 480
Db 421 AGTCCCTATAACACAGACCAACCGCAGAACACGCGTCAACGGCCCTTCGCCCTACGCACAG 480
QY 481 CCCAGTCCACCTTTCGATGCTCTCTCCATCAGCCGCCATCCCTCCCAACACCCAGTAC 540
Db 481 CCCAGTCCACCTTTCGATGCTCTCTCCATCAGCCGCCATCCCTCCCAACACCCAGTAC 540
QY 541 CCAGGCCCGCACAGTTTCGACGTGCTTCCAGCAGTTCGACACCGCCCAAGTCGGCCACC 600
Db 541 CCAGGCCCGCACAGTTTCGACGTGCTTCCAGCAGTTCGACACCGCCCAAGTCGGCCACC 600
QY 601 TGGACGTATTTCACCTGAATGAAGAACTCTACTGCAAAATTCGAAAGACATGCCCCATC 660
Db 601 TGGACGTATTTCACCTGAATGAAGAACTCTACTGCAAAATTCGAAAGACATGCCCCATC 660
QY 661 CAGATCAAGGTGATGACCCCACTCTCTCAGGAGCTGTTATCGCGCCATGCTGTCTAC 720
Db 661 CAGATCAAGGTGATGACCCCACTCTCTCAGGAGCTGTTATCGCGCCATGCTGTCTAC 720
QY 721 AAAAAAGCTGACGACGTACGAGGTTGTAAGCGGTGCGCCCAACCATGAGCTGAGCCGT 780
Db 721 AAAAAAGCTGACGACGTACGAGGTTGTAAGCGGTGCGCCCAACCATGAGCTGAGCCGT 780
QY 781 GAATTCACAGGGGACAGATTGCCCTCTCTAGTCAATTTGATTTCGAGTAGGGGAAACAGC 840
Db 781 GAATTCACAGGGGACAGATTGCCCTCTCTAGTCAATTTGATTTCGAGTAGGGGAAACAGC 840
QY 841 CATGCCCATGATGTAGAGATCCCATCAGAGAAAGACAGATGCTGTGATACCTTATGAG 900
Db 841 CATGCCCATGATGTAGAGATCCCATCAGAGAAAGACAGATGCTGTGATACCTTATGAG 900
QY 901 CCACCCCGAGTTGGCACTGAATTCAGCAGTCTTGTACAAATTTTCATGTGTAAACAGCAGT 960
Db 901 CCACCCCGAGTTGGCACTGAATTCAGCAGTCTTGTACAAATTTTCATGTGTAAACAGCAGT 960

[illegible]

RESULT 5

US-10-117-982-333

00 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1

Publication No. US20030138438A1

GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.

APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael

; APPLICANT: Mericle, Barbara

APPLICANT: Spies, Gregory A.

APPLICANT: Fan, Liqun

APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C18

; CURRENT APPLICATION NUMBER: US/10/117,982
 ;
 CURRENT FILING DATE: 2002-04-05

2002-04-05


```
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-117-982-333

Query Match      100.0%; Score 2816; DB 15; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTTGATATCAAGACAGATTGAAGGAAATGAAATTTTGAACATTCACGGTGTGCCACCT 60
DB 1 TCGTTGATATCAAGACAGATTGAAGGAAATGAAATTTTGAACATTCACGGTGTGCCACCT 60

QY 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTGG 120
DB 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTGG 120

QY 121 AAAGAAAGTTATTACCGATCCACCATGTCAGAGACACAGACAAATGAATTCCTCAGT 180
DB 121 AAAGAAAGTTATTACCGATCCACCATGTCAGAGACACAGACAAATGAATTCCTCAGT 180

QY 181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGAAACAGCCTATATGTTTCAGTTCAGCCC 240
DB 181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCTGAAACAGCCTATATGTTTCAGTTCAGCCC 240

QY 241 ATTGACTTGAACCTTTGTGGATGAACCATCAAGAGATGGTGGGACAAACAAGATTGAGATT 300
DB 241 ATTGACTTGAACCTTTGTGGATGAACCATCAAGAGATGGTGGGACAAACAAGATTGAGATT 300

QY 301 AGCATGAGCTGTATCCGATGCGAGCTCGGACTCGAGCTGAGTGCACCCCATGTGCGCACAGTAC 360
DB 301 AGCATGAGCTGTATCCGATGCGAGCTCGGACTCGAGCTGAGTGCACCCCATGTGCGCACAGTAC 360

QY 361 ACGAACTGGGGCTCTCTGAACAGCATGGACAGCAGATTGAGAAAGGCTCTCTGTCACAC 420
DB 361 ACGAACTGGGGCTCTCTGAACAGCATGGACAGCAGATTGAGAAAGGCTCTCTGTCACAC 420

QY 421 AGTCCCTATTAACACAGACCGGCGAGAACAGGTGACGGGGCTCTGCGCCCTAGGCACAG 480
DB 421 AGTCCCTATTAACACAGACCGGCGAGAACAGGTGACGGGGCTCTGCGCCCTAGGCACAG 480

QY 481 CCAGACTCCACCTTCGATGCTCTCTCATCCGCGCATCCCTTCCAAACCGACTAC 540
DB 481 CCAGACTCCACCTTCGATGCTCTCTCATCCGCGCATCCCTTCCAAACCGACTAC 540

QY 541 CCAGGCGCGCACAGTTTCGACGTGTCCTTCCAGCAGTCGAGCACCGCCAAAGTCGGCCACC 600
DB 541 CCAGGCGCGCACAGTTTCGACGTGTCCTTCCAGCAGTCGAGCACCGCCAAAGTCGGCCACC 600

QY 601 TGAACGTATTCACACTGAACCTGAAGAAACTCTACTGCCAAATTGGAAGACATGCCCATC 660
DB 601 TGAACGTATTCACACTGAACCTGAAGAAACTCTACTGCCAAATTGGAAGACATGCCCATC 660

QY 661 CAGATCAAGGTGATGACCCACCTCTCAGGAGCTGTTATCCGCGCATGCTCTGTCAC 720
DB 661 CAGATCAAGGTGATGACCCACCTCTCAGGAGCTGTTATCCGCGCATGCTCTGTCAC 720

QY 721 AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
DB 721 AAAAAAGCTGAGCACGTCACGGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780

QY 781 GAATTCACAGGGAACAGATTGCCCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC 840
DB 781 GAATTCACAGGGAACAGATTGCCCTCTAGTCAATTTGATTCGAGTAGAGGGGAACAGC 840

QY 841 CATGCCAGTATGTAGAAAGTCCCATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAG 900
DB 841 CATGCCAGTATGTAGAAAGTCCCATCACAGGAAGACAGAGTGTGCTGGTACCTTATGAG 900

QY 901 CCACCCAGGTTGGCACTGAATTCACGACAGTCTTGTGCAATTTTCATGTGTAAACAGCAGT 960
DB 901 CCACCCAGGTTGGCACTGAATTCACGACAGTCTTGTGCAATTTTCATGTGTAAACAGCAGT 960

961 CCACCCAGGTTGGCACTGAATTCACGACAGTCTTGTGCAATTTTCATGTGTAAACAGCAGT 960
961 TGTGTTGGAGGATGAACCGCGTCCAAATTTTAATCATTTGTTACTCTGGAACACAGAGAT 1020
961 TGTGTTGGAGGATGAACCGCGTCCAAATTTTAATCATTTGTTACTCTGGAACACAGAGAT 1020
1021 GGGCAAGTCTCTGGCGCAGCGCTGCTTTGAGGCCCGGATCTGTCTTGCCTCCAGGAAGAC 1080
1021 GGGCAAGTCTCTGGCGCAGCGCTGCTTTGAGGCCCGGATCTGTCTTGCCTCCAGGAAGAC 1080
1081 AGGAAGCGCGATGAAGATAGCATCAAGAAAGCAGCAAGTTTCGACAGTACAAAGAACCGT 1140
1081 AGGAAGCGCGATGAAGATAGCATCAAGAAAGCAGCAAGTTTCGACAGTACAAAGAACCGT 1140
1141 GATGTTACCAAGCGCGCTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
1141 GATGTTACCAAGCGCGCTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
1201 AAACGAAGATCCCCAGATGATGAATCTGTATATCTTACCAGTGAAGGCCGCTGAGACTTAT 1260
1201 AAACGAAGATCCCCAGATGATGAATCTGTATATCTTACCAGTGAAGGCCGCTGAGACTTAT 1260
1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGCACTACCTTCTCAGACACA 1320
1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACTCATGCACTACCTTCTCAGACACA 1320
1321 ATTGAACCTTACAGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
1321 ATTGAACCTTACAGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
1381 CTTTACGCTGCTTCAAGGAATGAGCTTGTGGAGCCCCGGAGAGAAACTCCAAACAACTCT 1440
1381 CTTTACGCTGCTTCAAGGAATGAGCTTGTGGAGCCCCGGAGAGAAACTCCAAACAACTCT 1440
1441 GAGCTCTTCTTAGACATTCAGAGCCCCCAACCGATCAAGTGTACCCATAGAGCCCTATC 1500
1441 GAGCTCTTCTTAGACATTCAGAGCCCCCAACCGATCAAGTGTACCCATAGAGCCCTATC 1500
1501 TCTATATTTAAGTGTGTGTTGTTATTTCCATGTATATGAGTGTGTGTGTGTGTGTGTGT 1560
1501 TCTATATTTAAGTGTGTGTTGTTATTTCCATGTATATGAGTGTGTGTGTGTGTGTGTGT 1560
1561 TGTGTGTGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620
1561 TGTGTGTGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620
1621 CCCAATGCTCAAAAGGCAAAAGCCACTAGTGAGAGAACTTTTGAAGGGACTCAAACT 1680
1621 CCCAATGCTCAAAAGGCAAAAGCCACTAGTGAGAGAACTTTTGAAGGGACTCAAACT 1680
1681 TTACAAAGAAAGGATGTTTTCAGATTTTGTATCTTACAGCCGCTTGGTGGGTGAG 1740
1681 TTACAAAGAAAGGATGTTTTCAGATTTTGTATCTTACAGCCGCTTGGTGGGTGAG 1740
1741 GAACCACTGTGTTGCTGTGAGCTTCTGTTGTTTCTGGAGGGAGGGGTGAGTGGG 1800
1741 GAACCACTGTGTTGCTGTGAGCTTCTGTTGTTTCTGGAGGGAGGGGTGAGTGGG 1800
1801 GAAGGGGATTTAAGATGTTTATGGAACCCCTTCTGCTTCTTCTGTTGTTTCTTAA 1860
1801 GAAGGGGATTTAAGATGTTTATGGAACCCCTTCTGCTTCTTCTGTTGTTTCTTAA 1860
1861 AATTCAAGGGAGCTTTTGAAGAGCTCTCAAACTTAAGATGCTTTTAAAGAAAGGAG 1920
1861 AATTCAAGGGAGCTTTTGAAGAGCTCTCAAACTTAAGATGCTTTTAAAGAAAGGAG 1920
1921 AAAAAAGTTGTTATGTTCTGTGCATAAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1980
1921 AAAAAAGTTGTTATGTTCTGTGCATAAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1980
1981 CCTTTTAAATGCTGTGTCATGTAATATNTTGAAGTAGTGAAGAAACGAAGGTGTCAGTG 2040
```


Db 1981 CCCTTTTAACCTCGTCAATGTAATAATATGCAAGTAGTAAGAAACGAAGGTGCAAGTG 2040
Qy TACTGCTGGGAGGAGGTGATCAATACCAAAAGTAATCAAACTTTGTGGTGGAGAGTTC 2100
Db TACTGCTGGGAGGAGGTGATCAATACCAAAAGTAATCAAACTTTGTGGTGGAGAGTTC 2100
Qy TTTGTGAGAACTTGCAATTAATTTGTGCTCTCCCTCATGTGTAGTGTAGTGTAGTGTAGT 2160
Db TTTGTGAGAACTTGCAATTAATTTGTGCTCTCCCTCATGTGTAGTGTAGTGTAGTGTAGT 2160
Qy GCTGTGTACCTGCTCTGCGCACTGTATGTGTGGCATCTGTATGTAAAGTTTTTCTTGTA 2220
Db GCTGTGTACCTGCTCTGCGCACTGTATGTGTGGCATCTGTATGTAAAGTTTTTCTTGTA 2220
Qy CATGAAACCCCTGGAGACCTACTACAAAAAATCTGTTGTTGGCCCCCATAGCAGGTGAA 2280
Db CATGAAACCCCTGGAGACCTACTACAAAAAATCTGTTGTTGGCCCCCATAGCAGGTGAA 2280
Qy CTCAATTTGTGCTTTTAATAGAAAGACAAATCCACCCAGTAATTAATGCGCTTACGTAGT 2340
Db CTCAATTTGTGCTTTTAATAGAAAGACAAATCCACCCAGTAATTAATGCGCTTACGTAGT 2340
Qy TGTGTACCAATTAATCAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTGTGATT 2400
Db TGTGTACCAATTAATCAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTGTGATT 2400
Qy AATTTGCTTAATAGAGCTTCTATCCCTCAAGCCTACCTACCATATAAACAGCCATATTA 2460
Db AATTTGCTTAATAGAGCTTCTATCCCTCAAGCCTACCTACCATATAAACAGCCATATTA 2460
Qy CTGATACCTGTTTCAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 2520
Db CTGATACCTGTTTCAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 2520
Qy AGAGCTGTTAAATACAGACTCTGAGCTGGAATTAAGAAATTAAGAAATTAAGAAATTA 2580
Db AGAGCTGTTAAATACAGACTCTGAGCTGGAATTAAGAAATTAAGAAATTAAGAAATTA 2580
Qy TTTCTTTTTTACTCAAAAGTTTAGAGAACTCTGTTTCTTTTCCATTTTAAACATATT 2640
Db TTTCTTTTTTACTCAAAAGTTTAGAGAACTCTGTTTCTTTTCCATTTTAAACATATT 2640
Qy TTAAGATAATAGCATAAAGACTTTAAATTTCTCTCCCTCCATCTTCCACACCCAGT 2700
Db TTAAGATAATAGCATAAAGACTTTAAATTTCTCTCCCTCCATCTTCCACACCCAGT 2700
Qy CACAGACTGTATTTCTGTACCAAGAAATTAATTTCTGTTTATGAGCTGTGCTT 2760
Db CACAGACTGTATTTCTGTACCAAGAAATTAATTTCTGTTTATGAGCTGTGCTT 2760
Qy TTTGATGATGTGATTTTAATTTTCAATAAATTTTGCATCTGTTTAAAGAA 2816
Db TTTGATGATGTGATTTTAATTTTCAATAAATTTTGCATCTGTTTAAAGAA 2816

RESULT 6

US-10-393-590-26
; Sequence 26, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human

US-10-393-590-26
Query Match 100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCGTTGATATCAAAAGACAGTTGAAGGAAATGAATTTTGAACATTTACGGTGTGCCACCT 60
Db 1 TCGTTGATATCAAAAGACAGTTGAAGGAAATGAATTTTGAACATTTACGGTGTGCCACCT 60
Qy 61 ACAGTACTGCCCTGACCCCTTACATTCAGCGCTTCGTAGAAACCCAGCTCATTTCTTTGG 120
Db 61 ACAGTACTGCCCTGACCCCTTACATTCAGCGCTTCGTAGAAACCCAGCTCATTTCTTTGG 120
Qy 121 AAAGAAAGTTTATTACCGATCCCATGTCCACAGACACAGACAAATGAATTCCTCAGT 180
Db 121 AAAGAAAGTTTATTACCGATCCCATGTCCACAGACACAGACAAATGAATTCCTCAGT 180
Qy 181 CCAGAGGTTTTCAGCATATATCTGGGATTTTCTGGAACAGCTTATATGTTTCAGTTCAGCCC 240
Db 181 CCAGAGGTTTTCAGCATATATCTGGGATTTTCTGGAACAGCTTATATGTTTCAGTTCAGCCC 240
Qy 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAGATGGTGGCAACAAAGATTGAGATT 300
Db 241 ATTGACTTGAACCTTTGTGGATGAACCATCAGAGATGGTGGCAACAAAGATTGAGATT 300
Qy 301 AGCATGAGCTGTATCCGATGCGAGTCCGAGCTCGGACCTGAGTGCACCCATGTGCCACAGTAC 360
Db 301 AGCATGAGCTGTATCCGATGCGAGTCCGAGCTCGGACCTGAGTGCACCCATGTGCCACAGTAC 360
Qy 361 ACAGAACTTGGGGTCTCTGAAACAGCATGGACAGCAGATTTCAGAACGGCTCTCTCGTCCACC 420
Db 361 ACAGAACTTGGGGTCTCTGAAACAGCATGGACAGCAGATTTCAGAACGGCTCTCTCGTCCACC 420
Qy 421 AGTCCCTTAACACAGACACCGCGAGAACAGCGTTCAGCGGCGCTCGCCCTACGCAAG 480
Db 421 AGTCCCTTAACACAGACACCGCGAGAACAGCGTTCAGCGGCGCTCGCCCTACGCAAG 480
Qy 481 CCAGCTCCACCTTCGATGCTCTCTCCATACCCGCGCATCCCTCCAAACCCAGCTAC 540
Db 481 CCAGCTCCACCTTCGATGCTCTCTCCATACCCGCGCATCCCTCCAAACCCAGCTAC 540
Qy 541 CCAGGCGCGCACAGTTTCGACGTGTCTCTCCAGCAGTTCGAGCACCGCCAAAGTGGCCACC 600
Db 541 CCAGGCGCGCACAGTTTCGACGTGTCTCTCCAGCAGTTCGAGCACCGCCAAAGTGGCCACC 600
Qy 601 TGACCTATTCACCTGAACTGAAGAAATCTCTAATGCAAAATTCGAAAGATGCCCCCATC 660
Db 601 TGACCTATTCACCTGAACTGAAGAAATCTCTAATGCAAAATTCGAAAGATGCCCCCATC 660
Qy 661 CAGATCAAGGTGATGACCCCTCTCAGGAGCTGTTATCCGCGCATGCGCTGTCTAC 720
Db 661 CAGATCAAGGTGATGACCCCTCTCAGGAGCTGTTATCCGCGCATGCGCTGTCTAC 720
Qy 721 AAAAAAGCTGAGCACGTCACGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
Db 721 AAAAAAGCTGAGCACGTCACGAGGTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
Qy 781 GAATTCAGAGGAGCAGATTGCCCCCTCTCTAGTCAATTTTCATGTTTAAACAGCAGT 840
Db 781 GAATTCAGAGGAGCAGATTGCCCCCTCTCTAGTCAATTTTCATGTTTAAACAGCAGT 840
Qy 841 CATGCCCCATGTAGAAAGTCCCATCAGAGGAGCAGAGTGTGCTGTTACCTTATGAG 900
Db 841 CATGCCCCATGTAGAAAGTCCCATCAGAGGAGCAGAGTGTGCTGTTACCTTATGAG 900
Qy 901 CCACCCAGGTTGGCACTGAATTCAGCAGCTCTGTACAAATTTTCATGTTTAAACAGCAGT 960
Db 901 CCACCCAGGTTGGCACTGAATTCAGCAGCTCTGTACAAATTTTCATGTTTAAACAGCAGT 960
Qy 961 TGTGTTGGAGGATGAACCCGCTCCAAATTTTAAATCATTTTAACTCTGGAACACAGAT 1020
Db 961 TGTGTTGGAGGATGAACCCGCTCCAAATTTTAAATCATTTTAACTCTGGAACACAGAT 1020

QY	1021	GGCAAGTCTCTGGCCGACGCTGCTTTGAGCCCGGATCTGCTGCTCCCGCAGGAGAGAC	1080
Db	1021	GGCAAGTCTCTGGCCGACGCTGCTTTGAGCCCGGATCTGCTGCTCCCGCAGGAGAGAC	1080
QY	1081	AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTACAAAGAACGGT	1140
Db	1081	AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTACAAAGAACGGT	1140
QY	1141	GATGGTAGAAGCGCCCGTTTTCGTCAGAACACACATGGTATCAGATGACATCATCAAG	1200
Db	1141	GATGGTAGAAGCGCCCGTTTTCGTCAGAACACACATGGTATCAGATGACATCATCAAG	1200
QY	1201	AAACGAGATCCCAGATGATGAATCTTATCTTACCAGTGAGGGCCGCTGAGACTTAT	1260
Db	1201	AAACGAGATCCCAGATGATGAATCTTATCTTACCAGTGAGGGCCGCTGAGACTTAT	1260
QY	1261	GAATGCTGTGAAGATCAAAAGTCCCTGGAACTCATGCAGTACCTTCTCAGCACACA	1320
Db	1261	GAATGCTGTGAAGATCAAAAGTCCCTGGAACTCATGCAGTACCTTCTCAGCACACA	1320
QY	1321	ATTGAACGTACAGGCNACAGCAACAGCAGCAGCACCGACCTTCTCAGAAACATCTC	1380
Db	1321	ATTGAACGTACAGGCNACAGCAACAGCAGCAGCACCGACCTTCTCAGAAACATCTC	1380
QY	1381	CTTTGAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAAACAACTCT	1440
Db	1381	CTTTGAGCCTGCTTCAGGAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAAACAACTCT	1440
QY	1441	GACGTCTTCTTTAGACATCCAAAGCCCCAAACCGATCAGTGAACCATAGAGCCCTATC	1500
Db	1441	GACGTCTTCTTTAGACATCCAAAGCCCCAAACCGATCAGTGAACCATAGAGCCCTATC	1500
QY	1501	TCATATTTTAAGTGTGTGTGTGTATTTCCATGTGTATATGTAGTGTGTGTGTGTGA	1560
Db	1501	TCATATTTTAAGTGTGTGTGTGTATTTCCATGTGTATATGTAGTGTGTGTGTGTGA	1560
QY	1561	TGTTGTGCTGTGTATCTAGCCCTCATAAACAGGACTTCAAGACACTTTGGCTCAGAGA	1620
Db	1561	TGTTGTGCTGTGTATCTAGCCCTCATAAACAGGACTTCAAGACACTTTGGCTCAGAGA	1620
QY	1621	CCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAACTTTTGAAGGGACTCAAACCT	1680
Db	1621	CCAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAACTTTTGAAGGGACTCAAACCT	1680
QY	1681	TTACAAAGAAAGATGTTTCTGAGATTTGTATCTTAGACCGGCCATTTGGTGGGTGAG	1740
Db	1681	TTACAAAGAAAGATGTTTCTGAGATTTGTATCTTAGACCGGCCATTTGGTGGGTGAG	1740
QY	1741	GAACCACTGTGTTGTCTGTGAGCTTCTGTTCTTCTGGGAGGGGTCAGGTGGG	1800
Db	1741	GAACCACTGTGTTGTCTGTGAGCTTCTGTTCTTCTGGGAGGGGTCAGGTGGG	1800
QY	1801	GAAAGGGCATTAAGATGTTTATGGAACCCCTTCTGCTTCTTCTGTTGTTTCTAA	1860
Db	1801	GAAAGGGCATTAAGATGTTTATGGAACCCCTTCTGCTTCTTCTGTTGTTTCTAA	1860
QY	1861	AATTCACAGGAGCTTTTTCAGCAGGCTCAAACTTAAGATGCTTTTAAAGAAAGGAG	1920
Db	1861	AATTCACAGGAGCTTTTTCAGCAGGCTCAAACTTAAGATGCTTTTAAAGAAAGGAG	1920
QY	1921	AAAAAGTTGTTTATGCTGTGCATTAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA	1980
Db	1921	AAAAAGTTGTTTATGCTGTGCATTAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA	1980
QY	1981	CCCTTTAATGCTGTCATGTAATAATATTGCAAGTAGTAAAGAAACGAAGTGTCAAGTG	2040
Db	1981	CCCTTTAATGCTGTCATGTAATAATATTGCAAGTAGTAAAGAAACGAAGTGTCAAGTG	2040
QY	2041	TACTGCTGGCCAGCGAGGTGATCATTTACCAAAAGTAATCAACTTTTGGTGGGTGAGATTTC	2100
Db	2041	TACTGCTGGCCAGCGAGGTGATCATTTACCAAAAGTAATCAACTTTTGGTGGGTGAGATTTC	2100

QY	2101	TTTGTGAGAACTTGCAATATTTTGTGTCTCCCTCATGTGTAGTAGAACAATTTCTTAAT	2160
Db	2101	TTTGTGAGAACTTGCAATATTTTGTGTCTCCCTCATGTGTAGTAGAACAATTTCTTAAT	2160
QY	2161	GCTGTGTACCTGCTCTGCGACCTGTATGTGGCATCTGTTATCTCTAAAGTTTTTCTTGTA	2220
Db	2161	GCTGTGTACCTGCTCTGCGACCTGTATGTGGCATCTGTTATCTCTAAAGTTTTTCTTGTA	2220
QY	2221	CATGAACCTCGGAAGACCTACTACAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAA	2280
Db	2221	CATGAACCTCGGAAGACCTACTACAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAA	2280
QY	2281	CTCATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCAGTAATATTGCCCTTACGTAGT	2340
Db	2281	CTCATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCAGTAATATTGCCCTTACGTAGT	2340
QY	2341	TGTTTACCATTATTTCAAAGCTCAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATT	2400
Db	2341	TGTTTACCATTATTTCAAAGCTCAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATT	2400
QY	2401	AATTTGCTTTAATTTAGAGCTTCTATCCCTCAAGCCTACCTACCAATAAAACAGCCATATTA	2460
Db	2401	AATTTGCTTTAATTTAGAGCTTCTATCCCTCAAGCCTACCTACCAATAAAACAGCCATATTA	2460
QY	2461	CTGATACCTGTTTCAGTGCATTTAGCCAGGAGACTTACGTTTGTAGTAAAGTGAGATCCAAAGC	2520
Db	2461	CTGATACCTGTTTCAGTGCATTTAGCCAGGAGACTTACGTTTGTAGTAAAGTGAGATCCAAAGC	2520
QY	2521	AGACGTGTTTAAATCAGACCTCTGCGACTGGAATTTAAAGATTTGAAAGGTGAGACTACTT	2580
Db	2521	AGACGTGTTTAAATCAGACCTCTGCGACTGGAATTTAAAGATTTGAAAGGTGAGACTACTT	2580
QY	2581	TTCTTTTCTTTTACTCAAAAGTTTAGAGAACTCTGTTTCTTCTTCAATTTTAAAAACATATT	2640
Db	2581	TTCTTTTCTTTTACTCAAAAGTTTAGAGAACTCTGTTTCTTCTTCAATTTTAAAAACATATT	2640
QY	2641	TTAAGATAATAGCATAAAGACTTTAAAAATGTTTCTCCCTCCATCTTCCACACCCAGT	2700
Db	2641	TTAAGATAATAGCATAAAGACTTTAAAAATGTTTCTCCCTCCATCTTCCACACCCAGT	2700
QY	2701	CACCAGCACTGATTTTCTGTCTACCAAGACAATGATTTCTTGTATTGAGGCTGTTGCTT	2760
Db	2701	CACCAGCACTGATTTTCTGTCTACCAAGACAATGATTTCTTGTATTGAGGCTGTTGCTT	2760
QY	2761	TTGTGGATGTGATTTTAAATTTCAATAAACTTTTGCACTTTGGTTTAAAAAGAAA	2816
Db	2761	TTGTGGATGTGATTTTAAATTTCAATAAACTTTTGCACTTTGGTTTAAAAAGAAA	2816

RESULT 7

US-10-393-590-27
; Sequence 27, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,789
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-590-27

Query Match 100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTTGATATCAAGACAGATTGAAGGAAATGAAATTTTGAACCTTCAACGGTGTGCCACCT 60
DB 1 TCGTTGATATCAAGACAGATTGAAGGAAATGAAATTTTGAACCTTCAACGGTGTGCCACCT 60
QY 61 ACAGTACTGCCCTTGACCCCTTACATCCAGCGTTTCGTAGAAAACCCAGAGCTCATTTCTCTGG 120
DB 61 ACAGTACTGCCCTTGACCCCTTACATCCAGCGTTTCGTAGAAAACCCAGAGCTCATTTCTCTGG 120
QY 121 AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACAACAAATGAAATTCCTCAGT 180
DB 121 AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACAACAAATGAAATTCCTCAGT 180
QY 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAAACAGCCTATATGTTTCAAGTTCCAGCC 240
DB 181 CCAGAGGTTTCCAGCATATCTGGGATTTTCTGGAAACAGCCTATATGTTTCAAGTTCCAGCC 240
QY 241 ATTCACTTGAACCTTTGTGGATGAACCATCAAGATGTTGGGACAGAAACAGATTTGAGATT 300
DB 241 ATTCACTTGAACCTTTGTGGATGAACCATCAAGATGTTGGGACAGAAACAGATTTGAGATT 300
QY 301 AGCATGGAATGTATCCGATCCAGGACTCGGACCTGAGTGAACCCCATGTGGCCACAGTAC 360
DB 301 AGCATGGAATGTATCCGATCCAGGACTCGGACCTGAGTGAACCCCATGTGGCCACAGTAC 360
QY 361 ACAGAACTGGGGCTCTGAACAGCATGGAACAGCAGATTCAGAACGGCTCTCTGTCAC 420
DB 361 ACAGAACTGGGGCTCTGAACAGCATGGAACAGCAGATTCAGAACGGCTCTCTGTCAC 420
QY 421 AGTCCCTATACACAGACCCGACAGAACAGCCTCAGGGCCCTCGCCCTACGCACAG 480
DB 421 AGTCCCTATACACAGACCCGACAGAACAGCCTCAGGGCCCTCGCCCTACGCACAG 480
QY 481 CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCGCCATCCCTCCACACGCACTAC 540
DB 481 CCCAGCTCCACCTTCGATGCTCTCTCTCCATCACCCGCCATCCCTCCACACGCACTAC 540
QY 541 CCAGGCCCGACAGTTTCGAGTGTCTCTTCAGCAGTCGAGCACCGCCAAAGTGGGCCACC 600
DB 541 CCAGGCCCGACAGTTTCGAGTGTCTCTTCAGCAGTCGAGCACCGCCAAAGTGGGCCACC 600
QY 601 TGGACGTATTCACCTGAACAACTGACCTTACTGCCAAATTCGAAAGACATGCCCATC 660
DB 601 TGGACGTATTCACCTGAACAACTGACCTTACTGCCAAATTCGAAAGACATGCCCATC 660
QY 661 CAGATCAAGGTGATGACCCACCTCTCAGGAGCTGTATCCCGCGCATGCCCTGTCTAC 720
DB 661 CAGATCAAGGTGATGACCCACCTCTCAGGAGCTGTATCCCGCGCATGCCCTGTCTAC 720
QY 721 AAAAAAGCTGACGACGTACGAGGTTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
DB 721 AAAAAAGCTGACGACGTACGAGGTTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGT 780
QY 781 GAATTCACAGGACAGATTGCCCTCTAGTCAATTTGATTGAGTAGAGGGGAAACAGC 840
DB 781 GAATTCACAGGACAGATTGCCCTCTAGTCAATTTGATTGAGTAGAGGGGAAACAGC 840
QY 841 CATGCCAGTATGTAGAAAGATCCCATCAAGGAGACAGAGTGTCTGGTACCTTATGAG 900
DB 841 CATGCCAGTATGTAGAAAGATCCCATCAAGGAGACAGAGTGTCTGGTACCTTATGAG 900
QY 901 CCACCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAAATTTTCATGTGTAAACAGAGT 960
DB 901 CCACCCAGGTTGGCACTGAATTCACGACAGTCTTGTACAAATTTTCATGTGTAAACAGAGT 960
QY 961 TGTGTTGGAGGATGAACCGCGTCCAAATTTTAAATCAATTTGATTCTCTGGAAACAGAGAT 1020
DB 961 TGTGTTGGAGGATGAACCGCGTCCAAATTTTAAATCAATTTGATTCTCTGGAAACAGAGAT 1020
QY 1021 GGGCAAGTCTTGGGCCAGCCTGCTTTGAGCCCGGATCTGTGCTTCCCGAGGAGAGAC 1080
DB 1021 GGGCAAGTCTTGGGCCAGCCTGCTTTGAGCCCGGATCTGTGCTTCCCGAGGAGAGAC 1080
QY 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTTCGACAGTACAAAGAACGGT 1140

DB 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGACAGTACAAAGAACGGT 1140
QY 1141 GATGGTACGAAGCGCCGCTTTCGTGAGAACACACATGATGATCCAGATGACATCCATCAAG 1200
DB 1141 GATGGTACGAAGCGCCGCTTTCGTGAGAACACACATGATGATCCAGATGACATCCATCAAG 1200
QY 1201 AAACGAAGATCCCCAGATGATGAACCTGTATATTTACCAGTGAGGGCCGTGAGACTTAT 1260
DB 1201 AAACGAAGATCCCCAGATGATGAACCTGTATATTTACCAGTGAGGGCCGTGAGACTTAT 1260
QY 1261 GAAATGCTGTTGAAGATCAAAAGAGTCCCTGGAACCTCATGAGTACCTTCCTCAGGACACA 1320
DB 1261 GAAATGCTGTTGAAGATCAAAAGAGTCCCTGGAACCTCATGAGTACCTTCCTCAGGACACA 1320
QY 1321 ATTGAAACGTFACAGGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
DB 1321 ATTGAAACGTFACAGGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
QY 1381 CTTTCAGCCTGCTTCAGGAAATGAGCTTTGTGGAGCCCGGAGAGAAACTCCAAAAACAATCT 1440
DB 1381 CTTTCAGCCTGCTTCAGGAAATGAGCTTTGTGAGCCCGGAGAGAAACTCCAAAAACAATCT 1440
QY 1441 GACGTCTTCTTTAGACATTCCAAAGCCCCAAAACCGATCAGTGTACCCATAGAGCCCTATC 1500
DB 1441 GACGTCTTCTTTAGACATTCCAAAGCCCCAAAACCGATCAGTGTACCCATAGAGCCCTATC 1500
QY 1501 TCTATATTTTAAAGTGTGTGTGTATTTCCATCTGTATATGTCAGTGTGTGTGTGTGTA 1560
DB 1501 TCTATATTTTAAAGTGTGTGTGTATTTCCATCTGTATATGTCAGTGTGTGTGTGTGTA 1560
QY 1561 TGTGTGTGCTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTTGGCTCAGAGA 1620
DB 1561 TGTGTGTGCTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTTGGCTCAGAGA 1620
QY 1621 CCCAACTGCTCAAAGGCAAAAGCCACTAGTGAGAGAACTCTTTTGAAGGACTCAAACCT 1680
DB 1621 CCCAACTGCTCAAAGGCAAAAGCCACTAGTGAGAGAACTCTTTTGAAGGACTCAAACCT 1680
QY 1681 TTACAAAGAAAGGATGTTTTCTGAGATTTTGTATCTTAGACCGCCATTTGGTGGGTGAG 1740
DB 1681 TTACAAAGAAAGGATGTTTTCTGAGATTTTCTGAGATTTTGTATCTTAGACCGCCATTTGGTGGGTGAG 1740
QY 1741 GAAACCACTGTGTTGTCTGTGAGCTTTCTGTGTTCTCGGAGGGGGGTCAAGTGGG 1800
DB 1741 GAAACCACTGTGTTGTCTGTGAGCTTTCTGTGTTCTCGGAGGGGGGTCAAGTGGG 1800
QY 1801 GAAAGGGGCAATTAAGATGTTTATTGGAAACCTTTTCTGCTCTCTTTCTTTCTAA 1860
DB 1801 GAAAGGGGCAATTAAGATGTTTATTGGAAACCTTTTCTGCTCTCTTTCTTTCTAA 1860
QY 1861 AATTCACAGGAAAGCTTTTGAGCAGGCTTCAAACTTAAGATGCTTTTTTAAGAAAAAGAG 1920
DB 1861 AATTCACAGGAAAGCTTTTGAGCAGGCTTCAAACTTAAGATGCTTTTTTAAGAAAAAGAG 1920
QY 1921 AAAAAAGTTGTTATTGTCTGTGATTAAGTAAGTTGTAAGTGAAGTGAAGTGAAGTGAAGT 1980
DB 1921 AAAAAAGTTGTTATTGTCTGTGATTAAGTAAGTTGTAAGTGAAGTGAAGTGAAGTGAAGT 1980
QY 1981 CCCTTTTAATGCTGGTCACTGAATAATATTGCAAGTAGTAAGAAACGAAGGTGCAAGTG 2040
DB 1981 CCCTTTTAATGCTGGTCACTGAATAATATTGCAAGTAGTAAGAAACGAAGGTGCAAGTG 2040
QY 2041 TACTGCTGGGACGAGGAGTCAATTTACCAAAAGTAACTTTTGGTGGGTGGAGAGTTT 2100
DB 2041 TACTGCTGGGACGAGGAGTCAATTTACCAAAAGTAACTTTTGGTGGGTGGAGAGTTT 2100
QY 2101 TTTGTGAGAACTTGCATTTATTTGTGCTCCCTCATGTGTAGGTAGAACATTTCTTAAT 2160
DB 2101 TTTGTGAGAACTTGCATTTATTTGTGCTCCCTCATGTGTAGGTAGAACATTTCTTAAT 2160
QY 2161 GCTGTGTAACCTGCTCTGCGACCTGTATGTTGGCACTGTGTTATGCTAAAGTTTTTCTGTA 2220

1201 AACGAGATCCCGAGATGATGAACCTGTTATATCTTACCAGTGAGGGGCGGTGAGACTTAT 1260
1201 AACGAGATCCCGAGATGATGAACCTGTTATATCTTACCAGTGAGGGGCGGTGAGACTTAT 1260
1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTATGAGTACCTTCCCTCAGCAGACA 1320
1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAACCTATGAGTACCTTCCCTCAGCAGACA 1320
1321 ATTGAACGTTACAGGCAACAGCAAGCAGAGCAGACACCTTACTTTCAGAAACATCTC 1380
1321 ATTGAACGTTACAGGCAACAGCAAGCAGAGCAGACACCTTACTTTCAGAAACATCTC 1380
1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGAGCCCGGAGAGAACTCCAAACAACTCT 1440
1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGAGCCCGGAGAGAACTCCAAACAACTCT 1440
1441 GACGTCTCTTTAGACATTCAGCCCTCATAAACAGGACTTTGAAGACACTTTTGGCTCAGAGA 1500
1441 GACGTCTCTTTAGACATTCAGCCCTCATAAACAGGACTTTGAAGACACTTTTGGCTCAGAGA 1500
1501 TCTATATTTTAAAGTGTGTGTTGATTTCCATGTATATGTGAGTGTGTGTGTGTA 1560
1501 TCTATATTTTAAAGTGTGTGTTGATTTCCATGTATATGTGAGTGTGTGTGTGTA 1560
1561 TGTGTGTCGTGTGTATCTAGCCCTCATAAACAGGACTTTGAAGACACTTTTGGCTCAGAGA 1620
1561 TGTGTGTCGTGTGTATCTAGCCCTCATAAACAGGACTTTGAAGACACTTTTGGCTCAGAGA 1620
1621 CCCAACTGCTCAAAAGGCACAAAGCCACTAGTGTGAGAAATCTTTTGAAGGACTCAAACT 1680
1621 CCCAACTGCTCAAAAGGCACAAAGCCACTAGTGTGAGAAATCTTTTGAAGGACTCAAACT 1680
1681 TTACAAGAAAGGATGTTTCTGAGATTTTCTGATCTTACCGGCAATCTGTCGGGTGAG 1740
1681 TTACAAGAAAGGATGTTTCTGAGATTTTCTGATCTTACCGGCAATCTGTCGGGTGAG 1740
1741 GAACCACTGTTTGTCTGTGAGCTTCTGTTGTTTCTCGGAGGGGGTCAAGTGGG 1800
1741 GAACCACTGTTTGTCTGTGAGCTTCTGTTGTTTCTCGGAGGGGGTCAAGTGGG 1800
1801 GAAAGGGGCATTAAGATGTTTATTTGGAACCTTTTCTGCTCTCTTCTGTTGTTTCTTAA 1860
1801 GAAAGGGGCATTAAGATGTTTATTTGGAACCTTTTCTGCTCTCTTCTGTTGTTTCTTAA 1860
1861 AATTACAGGGAAGCTTTTGAAGGAGCTCTCAACTTAAGATGTTCTTTTAAAGAAAGGAG 1920
1861 AATTACAGGGAAGCTTTTGAAGGAGCTCTCAACTTAAGATGTTCTTTTAAAGAAAGGAG 1920
1921 AAAAAAGTTGTTATTTGCTGTCATAGTAAGTTGTAGTGACTGAGAGACTCAGTCAGA 1980
1921 AAAAAAGTTGTTATTTGCTGTCATAGTAAGTTGTAGTGACTGAGAGACTCAGTCAGA 1980
1981 CCCTTTTAACTGCTGTCATGTAATTAATTCAGAGTGTAGTAAGAAACGAGGTGCAAGTG 2040
1981 CCCTTTTAACTGCTGTCATGTAATTAATTCAGAGTGTAGTAAGAAACGAGGTGCAAGTG 2040
2041 TACTGCTGGGCGAGGTGATCAATACCAAAAGTCACTTGTGGTGGAGAGTTC 2100
2041 TACTGCTGGGCGAGGTGATCAATACCAAAAGTCACTTGTGGTGGAGAGTTC 2100
2101 TTTGTGAGAACTTGCATTTATTTGTCCTCCCTCATGTGTAGGTAGAACATTTTCTTAAT 2160
2101 TTTGTGAGAACTTGCATTTATTTGTCCTCCCTCATGTGTAGGTAGAACATTTTCTTAAT 2160
2161 GCTGTGACCTGCTCTGCGCACTGTATGTTGGCATCTGTATAGCTTAAAGTTTTTCTGTGA 2220
2161 GCTGTGACCTGCTCTGCGCACTGTATGTTGGCATCTGTATAGCTTAAAGTTTTTCTGTGA 2220
2221 CATGAAACCCCTGGAAGACCTACTACAAAAAATCTGTTGTTGGCCCCCATAGCAGGTGAA 2280
2221 CATGAAACCCCTGGAAGACCTACTACAAAAAATCTGTTGTTGGCCCCCATAGCAGGTGAA 2280

2281 CTCATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCAGTAATATTTCCCTTACGTAGT 2340
2281 CTCATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCAGTAATATTTCCCTTACGTAGT 2340
2341 TGTTACCATTTTCAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAANAATCTGTGATT 2400
2341 TGTTACCATTTTCAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAANAATCTGTGATT 2400
2401 AATTGTCTTAAATAGAGCTTCTATCCCTCAAGCCCTACCTACCATAAAAACAGCCATATTA 2460
2401 AATTGTCTTAAATAGAGCTTCTATCCCTCAAGCCCTACCTACCATAAAAACAGCCATATTA 2460
2461 CTGATACCTGTTCAAGTGCATTTAGCCAGAGACTTTACGTTTGTAGTAAAGTGAAGTCCAAAGC 2520
2461 CTGATACCTGTTCAAGTGCATTTAGCCAGAGACTTTACGTTTGTAGTAAAGTGAAGTCCAAAGC 2520
2521 AGAGCTGTTAAATCAGACACTCTCGGACTCGGAATTTAAAGATTTAAAGGGTAGACTACTT 2580
2521 AGAGCTGTTAAATCAGACACTCTCGGACTCGGAATTTAAAGATTTAAAGGGTAGACTACTT 2580
2581 TTCTTTTCTTACTCCTCAAAAGTCTAGAGAACTCTCTGTTTCTTCTTCCATTTTAAAAACATATT 2640
2581 TTCTTTTCTTACTCCTCAAAAGTCTAGAGAACTCTCTGTTTCTTCTTCCATTTTAAAAACATATT 2640
2641 TTAAGATAATAGCATAAAGACTTTTAAAAATGTTCCCTCCCTCCATCTTCCACACCCAGT 2700
2641 TTAAGATAATAGCATAAAGACTTTTAAAAATGTTCCCTCCCTCCATCTTCCACACCCAGT 2700
2701 CACCAGCACTGATTTTCTGTCACCAAGACAAATGATTTCTGTTTATTGAGGCTGTGCTT 2760
2701 CACCAGCACTGATTTTCTGTCACCAAGACAAATGATTTCTGTTTATTGAGGCTGTGCTT 2760
2761 TTGTGGATGTGATTTTAAATTTTCAATAAATTTTGCATCTTGGTTTAAAAAGAAA 2816
2761 TTGTGGATGTGATTTTAAATTTTCAATAAATTTTGCATCTTGGTTTAAAAAGAAA 2816

RESULT 9

US-10-393-590-65
; Sequence 65, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO
; FILE REFERENCE: CDS 268 US NP
; CURRENT APPLICATION NUMBER: US/10/393,590
; CURRENT FILING DATE: 2003-03-21
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-590-65

Query Match 100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTTGATATCAAAAGACAGTTGAAGGAAATGAATTTTGAACCTTTCACGGTGTGCCACCT 60
Db 1 TCGTTGATATCAAAAGACAGTTGAAGGAAATGAATTTTGAACCTTTCACGGTGTGCCACCT 60
Qy 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAAACCCAGCTCATTTCTCTGG 120
Db 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAAACCCAGCTCATTTCTCTGG 120
Qy 121 AAAGAAAGTTATTACCGATCCCATGTCCAGAGCACAGACAAATGAATTTCTCTCAGT 180
Db 121 AAAGAAAGTTATTACCGATCCCATGTCCAGAGCACAGACAAATGAATTTCTCTCAGT 180


```
QY 1381 CTTTCAGCTGCTTCAGGAATGAGCTTGTTGGAGCCCGGAGAGAAAATCCAAACAATCT 1440
DB 1381 CTTTCAGCTGCTTCAGGAATGAGCTTGTTGGAGCCCGGAGAGAAAATCCAAACAATCT 1440
QY 1441 GAGCTCTCTTTAGACATTCGAAGCCCAAAACCGATCAGTGATCCCATAGAGCCCTATC 1500
DB 1441 GAGCTCTCTTTAGACATTCGAAGCCCAAAACCGATCAGTGATCCCATAGAGCCCTATC 1500
QY 1501 TCTATATTTTAAAGTGCTGTTCTGATTTCCATGTTATATGAGTGCTGTTGGTGA 1560
DB 1501 TCTATATTTTAAAGTGCTGTTCTGATTTCCATGTTATATGAGTGCTGTTGGTGA 1560
QY 1561 TGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTTGAAGACACTTTGGCTCAGAGA 1620
DB 1561 TGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTTGAAGACACTTTGGCTCAGAGA 1620
QY 1621 CCNACTGCTCAAAAGGCACAAAGCCACTAGTGAGAGAAATCTTTTGAAGGAGCTCAAACT 1680
DB 1621 CCNACTGCTCAAAAGGCACAAAGCCACTAGTGAGAGAAATCTTTTGAAGGAGCTCAAACT 1680
QY 1681 TTACAAGAAAGGATGTTTCTGCAGATTTGTATCTTAGACCGCCATTGGTGGTGAG 1740
DB 1681 TTACAAGAAAGGATGTTTCTGCAGATTTGTATCTTAGACCGCCATTGGTGGTGAG 1740
QY 1741 GAACCACTGTGTTGCTGTGAGCTTTCTGTTGTTCTCGGAGGGAGGGTCAAGTGGG 1800
DB 1741 GAACCACTGTGTTGCTGTGAGCTTTCTGTTGTTCTCGGAGGGAGGGTCAAGTGGG 1800
QY 1801 GAAAGGGGCATTAAGATGTTTATGGAAACCTTTTCTGCTCTCTCTGTTGTTTCTAA 1860
DB 1801 GAAAGGGGCATTAAGATGTTTATGGAAACCTTTTCTGCTCTCTCTGTTGTTTCTAA 1860
QY 1861 AATTCACAGGAGCTTTTGGAGGAGTCTCAAACTTAAGATGCTTTTGAAGAAAGGAG 1920
DB 1861 AATTCACAGGAGCTTTTGGAGGAGTCTCAAACTTAAGATGCTTTTGAAGAAAGGAG 1920
QY 1921 AAAAAAGTGTGTTGCTGTGATAGTAAAGTGTAGTGACTGAGAGACTCAGTCAGA 1980
DB 1921 AAAAAAGTGTGTTGCTGTGATAGTAAAGTGTAGTGACTGAGAGACTCAGTCAGA 1980
QY 1981 CCCTTTTAAATGCTGCTCATGTAATATATTCGAAGTAGTAAGAACGAAGGTGCAAGTG 2040
DB 1981 CCCTTTTAAATGCTGCTCATGTAATATATTCGAAGTAGTAAGAACGAAGGTGCAAGTG 2040
QY 2041 TACTGCTGGCAGCGAGTGTATCTACCAAAAGTAACTTTTGGGTGGAGAGTTC 2100
DB 2041 TACTGCTGGCAGCGAGTGTATCTACCAAAAGTAACTTTTGGGTGGAGAGTTC 2100
QY 2101 TTTGTGAGAACTTGCAATATTTGTGCTCCTCCCTCATGTGTAGGTAGAACATTTCTTAAT 2160
DB 2101 TTTGTGAGAACTTGCAATATTTGTGCTCCTCCCTCATGTGTAGGTAGAACATTTCTTAAT 2160
QY 2161 GCTGTGTACCTGCTCTGCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTCTTGTA 2220
DB 2161 GCTGTGTACCTGCTCTGCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTCTTGTA 2220
QY 2221 CATGAACCTGGAGACCTACTACAAAAGAACTGTTGTTGGCCCTCCATAGCAGGTGAA 2280
DB 2221 CATGAACCTGGAGACCTACTACAAAAGAACTGTTGTTGGCCCTCCATAGCAGGTGAA 2280
QY 2281 CTCAATTTGTGCTTTTAAAGAAAGACAAATCCACCCAGTAAATATTTGCCCTTACGTAGT 2340
DB 2281 CTCAATTTGTGCTTTTAAAGAAAGACAAATCCACCCAGTAAATATTTGCCCTTACGTAGT 2340
QY 2341 TGTTTACCAATTTCAAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTGTGATT 2400
DB 2341 TGTTTACCAATTTCAAAGCTCAAAATAGAAATTTGAAGCCCTCTCACAAAATCTGTGATT 2400
QY 2401 AATTTGCTTAATAGAGCTTCTATCCCTCAAGCTTACTACCATAAACAGCCATATTA 2460
DB 2401 AATTTGCTTAATAGAGCTTCTATCCCTCAAGCTTACTACCATAAACAGCCATATTA 2460
```

RESULT 11

```
US-10-393-567-27
; Sequence 27, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-567-27
```

```
Query Match 100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCTTGATATCAAGACAGTGAAGGAAATGAATTTTGAACCTTCACGGTGTGCCACCT 60
DB 1 TCCTTGATATCAAGACAGTGAAGGAAATGAATTTTGAACCTTCACGGTGTGCCACCT 60
QY 61 ACAGTACTGCCCTGACCTTTACATCAGCGTTTCGTAGAACCCAGCTCAATTTCTCTGG 120
DB 61 ACAGTACTGCCCTGACCTTTACATCAGCGTTTCGTAGAACCCAGCTCAATTTCTCTGG 120
QY 121 AAAGAAGTTATTACCGATCCACATGTCCAGAGCACACAGACAAATGAATTCCTCAGT 180
DB 121 AAAGAAGTTATTACCGATCCACATGTCCAGAGCACACAGACAAATGAATTCCTCAGT 180
QY 181 CCAGAGTTTTCAGCATATCTGGGATTTTCTGGAAACAGCCTATATGTTTCAGTTCAGCCC 240
DB 181 CCAGAGTTTTCAGCATATCTGGGATTTTCTGGAAACAGCCTATATGTTTCAGTTCAGCCC 240
QY 241 ATTGACTTGAACCTTTTGGATGAACCATCAGAAGATGGTGGCGAACAACAGATTGAGATT 300
DB 241 ATTGACTTGAACCTTTTGGATGAACCATCAGAAGATGGTGGCGAACAACAGATTGAGATT 300
QY 301 AGCATGGACTGTATCCGATCGAGGACTCGGACCTGAGTACCCCATGTGCCACAGTAC 360
DB 301 AGCATGGACTGTATCCGATCGAGGACTCGGACCTGAGTACCCCATGTGCCACAGTAC 360
```

QY 361 ACGAACCTGGGGCTCCTGAAACAGCATGGAACAGACAGATTCAGAACGGCTCCTCGTCCACC 420
DB 361 ACGAACCTGGGGCTCCTGAAACAGCATGGAACAGACAGATTCAGAACGGCTCCTCGTCCACC 420
QY 421 AGTCCCTATAACACAGACACCGCAGAACAGCGTCAAGCGGCCCTCGCCCTAGCCACAG 480
DB 421 AGTCCCTATAACACAGACACCGCAGAACAGCGTCAAGCGGCCCTCGCCCTAGCCACAG 480
QY 481 CCCAGCTCCACTTCGATGCTCTCTCCATCACCCCGCATCCCTCCAAACACCGACTAC 540
DB 481 CCCAGCTCCACTTCGATGCTCTCTCCATCACCCCGCATCCCTCCAAACACCGACTAC 540
QY 541 CCAGCGCCGACAGTTTCGACGTGCTCTTCAGACAGTCGACGACCGCCAAAGTCGGCCACC 600
DB 541 CCAGCGCCGACAGTTTCGACGTGCTCTTCAGACAGTCGACGACCGCCAAAGTCGGCCACC 600
QY 601 TGGACGTATTCACCTGAACTCAAGAACTCTACTGCCAAATTCGAAAGACATGCCCATC 660
DB 601 TGGACGTATTCACCTGAACTCAAGAACTCTACTGCCAAATTCGAAAGACATGCCCATC 660
QY 661 CAGATCAAGGTGATGACCCCACTCCTCAGGGAGCTGTTATCCGCGCATGCCCTGTCTAC 720
DB 661 CAGATCAAGGTGATGACCCCACTCCTCAGGGAGCTGTTATCCGCGCATGCCCTGTCTAC 720
QY 721 AAAAAAGCTGACGCTACCGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT 780
DB 721 AAAAAAGCTGACGCTACCGGAGGTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCCGT 780
QY 781 GAATTCACAGGACAGATGGCCCTCCTAGTCAATTTGATTCAGTAGAGGGAACAGC 840
DB 781 GAATTCACAGGACAGATGGCCCTCCTAGTCAATTTGATTCAGTAGAGGGAACAGC 840
QY 841 CATGCCAGTATGTAAGATGCCCATCACAGGAAGACAGAGTGTGCTGCTACCTTATGAG 900
DB 841 CATGCCAGTATGTAAGATGCCCATCACAGGAAGACAGAGTGTGCTGCTACCTTATGAG 900
QY 901 CCACCCAGGTGGCACTGAATTCACGACAGCTTTGTACAAATTTTCATGTGTAAACAGCAGT 960
DB 901 CCACCCAGGTGGCACTGAATTCACGACAGCTTTGTACAAATTTTCATGTGTAAACAGCAGT 960
QY 961 TGTGTTGGAGGATGAACCCGCTCCAAATTTAATCATTTGTTACTCTGGAACCCAGAGAT 1020
DB 961 TGTGTTGGAGGATGAACCCGCTCCAAATTTAATCATTTGTTACTCTGGAACCCAGAGAT 1020
QY 1021 GGGCAAGTCTCGGCCGACGCTGCTTTGAGGCCCGGATCTGTGCTCCCGCAGGAAGAGAC 1080
DB 1021 GGGCAAGTCTCGGCCGACGCTGCTTTGAGGCCCGGATCTGTGCTCCCGCAGGAAGAGAC 1080
QY 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGACCGGT 1140
DB 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTCGGACAGTACAAAGACCGGT 1140
QY 1141 GATGGTACGAAGCCCGTTTCGTCAGAAACACATGGTATCCAGATGACATCCATCAAG 1200
DB 1141 GATGGTACGAAGCCCGTTTCGTCAGAAACACATGGTATCCAGATGACATCCATCAAG 1200
QY 1201 AAACGAAGATCCCAGATGATGAATCTGTTATCTTACAGTGGGGCCGTGAGACTTAT 1260
DB 1201 AAACGAAGATCCCAGATGATGAATCTGTTATCTTACAGTGGGGCCGTGAGACTTAT 1260
QY 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAATCTATGAGTACCTTCTCAGCACACA 1320
DB 1261 GAAATGCTGTTGAAGATCAAGAGTCCCTGGAATCTATGAGTACCTTCTCAGCACACA 1320
QY 1321 ATTGAACGTTACAGGCAACAGCAACAGCAGGACCAAGCACTTATTCAGAAACATCTC 1380
DB 1321 ATTGAACGTTACAGGCAACAGCAACAGCAGGACCAAGCACTTATTCAGAAACATCTC 1380
QY 1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGAGCCCGGAGAGAACTCCAAACCAATCT 1440
DB 1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGAGCCCGGAGAGAACTCCAAACCAATCT 1440
QY 1441 GACGTCTCTTTAGACATTCGAAGCCCCCAACCGATCAGTGTACCCATAGAGCCCTATC 1500

DB 1441 GACGTCTCTTTAGACATTCGAAGCCCCCAACCGATCAGTGTACCCATAGAGCCCTATC 1500
QY 1501 TCTATATTTTAAAGTGTGTGTTGTTATTTCCATGTGTATATGTAGTGTGTGTGTGTA 1560
DB 1501 TCTATATTTTAAAGTGTGTGTGTTATTTCCATGTGTATATGTAGTGTGTGTGTGTA 1560
QY 1561 TGTGTGCGCTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTTGGCTCAGAGA 1620
DB 1561 TGTGTGCGCTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTTGGCTCAGAGA 1620
QY 1621 CCMAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAACTTTTTGAAGGGACTCAAACCT 1680
DB 1621 CCMAACTGCTCAAAGGCACAAAGCCACTAGTGAGAGAACTTTTTGAAGGGACTCAAACCT 1680
QY 1681 TTACAAGAAAGGATGTTTTCTGCAGATTTTGTATCCTTAGACCGGCCATTTGGTGGGTGAG 1740
DB 1681 TTACAAGAAAGGATGTTTTCTGCAGATTTTGTATCCTTAGACCGGCCATTTGGTGGGTGAG 1740
QY 1741 GAACCACTGTGTTTGTCTGTGAGCTTTCTGTGTTTCTGGGAGGGGCTCAGGTGGG 1800
DB 1741 GAACCACTGTGTTTGTCTGTGAGCTTTCTGTGTTTCTGGGAGGGGCTCAGGTGGG 1800
QY 1801 GAAAGGGGCATTAAGATGTTTATTGGAAACCCCTTTTCTGTCTTCTTGTGTTTTCTTAA 1860
DB 1801 GAAAGGGGCATTAAGATGTTTATTGGAAACCCCTTTTCTGTCTTCTTGTGTTTTCTTAA 1860
QY 1861 AATTTCACAGGAAGCTTTTGACGAGCTCTCAAACTTAAGATGCTCTTTTAAAGAAAGGAG 1920
DB 1861 AATTTCACAGGAAGCTTTTGACGAGCTCTCAAACTTAAGATGCTCTTTTAAAGAAAGGAG 1920
QY 1921 AAAAAAGTTGTTATTTGTCTGTGATTAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA 1980
DB 1921 AAAAAAGTTGTTATTTGTCTGTGATTAAGTAAGTTGTAGGTGACTGAGAGACTCAGTCAGA 1980
QY 1981 CCCTTTTAAATGCTGGTCACTGTAATAATATTGCAAGTAGTAAGAAACGAAGGTGTCAAAGTG 2040
DB 1981 CCCTTTTAAATGCTGGTCACTGTAATAATATTGCAAGTAGTAAGAAACGAAGGTGTCAAAGTG 2040
QY 2041 TACTGTGGGACGAGGTGATCATTTACCAAAAAGTAACTCACTTTTGGGTGGAGAGTTT 2100
DB 2041 TACTGTGGGACGAGGTGATCATTTACCAAAAAGTAACTCACTTTTGGGTGGAGAGTTT 2100
QY 2101 TTTGTGAGAACTTGTCAATTTTGTGCTCCTCCCTCATGTGTAGGTAGAACATTTCTTAAAT 2160
DB 2101 TTTGTGAGAACTTGTCAATTTTGTGCTCCTCCCTCATGTGTAGGTAGAACATTTCTTAAAT 2160
QY 2161 GCTGTGTACCTGCTCTGCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCTTGTGA 2220
DB 2161 GCTGTGTACCTGCTCTGCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCTTGTGA 2220
QY 2221 CATGAACCCCTGGAAGACCTTACTACAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAA 2280
DB 2221 CATGAACCCCTGGAAGACCTTACTACAAAAAACTGTTGTTGGCCCCCATAGCAGGTGAA 2280
QY 2281 CTCAATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCAGTAATATTGCCCTTACGTAGT 2340
DB 2281 CTCAATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCAGTAATATTGCCCTTACGTAGT 2340
QY 2341 TGTTTACCATTTTCAAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATTT 2400
DB 2341 TGTTTACCATTTTCAAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATTT 2400
QY 2401 AATTTCCTTAAATPAGAGCTTCTATCCCTCAAGCCTACCTACCATAAAACAGCCATATTA 2460
DB 2401 AATTTCCTTAAATPAGAGCTTCTATCCCTCAAGCCTACCTACCATAAAACAGCCATATTA 2460
QY 2461 CTGATACTGTTCAAGTGCATTTAGCCAGGAGACTTACGTTTTGAGTAAAGTGAAGTCCAAAGC 2520
DB 2461 CTGATACTGTTCAAGTGCATTTAGCCAGGAGACTTACGTTTTGAGTAAAGTGAAGTCCAAAGC 2520
QY 2521 AGACGTGTTTAAATCAGCACTCCTGACCTGGAAATTTAAAGATTTGAAGGGGTAGACTACTT 2580

Db 2521 AGACGTGTTAAATACAGCACTCTCGAGCTGGAAATTAAGATTGAAAGGCTAGACTACTT 2580
Qy TTCTTTTTTTTTTACTCAAAAGTTTAGAGAACTCTCTGTTTCTTTCCATTTTAAACATATT 2640
Db TTTCTTTTTTTTTTACTCAAAAGTTTAGAGAACTCTCTGTTTCTTTCCATTTTAAACATATT 2640
Qy TTAAGATAAATAGCATAAAGACTTTTAAAAATGTTTCTCTCCCTCCATCTTCCACACCCAGT 2700
Db TTAAGATAAATAGCATAAAGACTTTTAAAAATGTTTCTCTCCCTCCATCTTCCACACCCAGT 2700
Qy CACCAGCACTGATTTTCTGTCCACCAAGCAATGATTTCTGTTATTTAGGCTGTTGCTT 2760
Db CACCAGCACTGATTTTCTGTCCACCAAGCAATGATTTCTGTTATTTAGGCTGTTGCTT 2760
Qy TTGTTGATGTGATTTTAAATTTTCAATAAACTTTTGCATCTTGGTTTAAAGAAA 2816
Db TTGTTGATGTGATTTTAAATTTTCAATAAACTTTTGCATCTTGGTTTAAAGAAA 2816

RESULT 12
US-10-393-567-64
; Sequence 64, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-393-567-64

Query Match 100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTTGATATCAAAAGCAGTTGAAGGAAATGAAATTTTGAACATTCACGGTGTGCCACCT 60
Db 1 TCGTTGATATCAAAAGCAGTTGAAGGAAATGAAATTTTGAACATTCACGGTGTGCCACCT 60
Qy 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTGG 120
Db 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCCAGCTCATTTCTCTGG 120
Qy 121 AAAGAAAGTTATTACCGATCCACATGTCCTCAGAGCACAGACAATGAATTCCTCAGT 180
Db 121 AAAGAAAGTTATTACCGATCCACATGTCCTCAGAGCACAGACAATGAATTCCTCAGT 180
Qy 181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCGGAACAGCTATATGTTTCAGTTCAGCCC 240
Db 181 CCAGAGGTTTTCCAGCATATCTGGGATTTTCGGAACAGCTATATGTTTCAGTTCAGCCC 240
Qy 241 ATTGACTTTGAACCTTTGTGGATGAACCATCAAGAGATGGTGGCAAAACAAGATTGAGATT 300
Db 241 ATTGACTTTGAACCTTTGTGGATGAACCATCAAGAGATGGTGGCAAAACAAGATTGAGATT 300
Qy 301 AGCATGGACTGATCCCGATCGAGGACTCGGACTGAGTGCACCCCATGTGCCACAGTAC 360
Db 301 AGCATGGACTGATCCCGATCGAGGACTCGGACTGAGTGCACCCCATGTGCCACAGTAC 360
Qy 361 ACGAACCTGGGGTCTCTGAACAGCATGGCAGCAGATTCAGAACGGCTCTCTGTCACC 420
Db 361 ACGAACCTGGGGTCTCTGAACAGCATGGCAGCAGATTCAGAACGGCTCTCTGTCACC 420
Qy 421 AGTCCCTTAAACACAGACCCAGCGTCAAGCGTCAAGCGGCTCGCCCTACGCACAG 480
Db TTTCTTTTTTTTTTACTCAAAAGTTTAGAGAACTCTCTGTTTCTTTCCATTTTAAACATATT

Db 421 AGTCCCTTAAACACAGACCCAGCGCAGAAACAGCGTCAAGCGGCCCTCGCCCTACGCACAG 480
Qy CCAGCTCCACACCTTCGATGCTCTCTCTCATACACCGCCCATCCCTCCACACCGACTAC 540
Db CCAGCTCCACACCTTCGATGCTCTCTCTCATACACCGCCCATCCCTCCACACCGACTAC 540
Qy CCAGGCCCGCAGAGTTTCGACGTTCTTCCAGCAGTCGAGCACCCCAAGTCGGCCACC 600
Db CCAGGCCCGCAGAGTTTCGACGTTCTTCCAGCAGTCGAGCACCCCAAGTCGGCCACC 600
Qy TGGACGTTATTCACCTGAACTGAAGAACTCTACTGCAAAATTCGAAGACATGCCCCATC 660
Db TGGACGTTATTCACCTGAACTGAAGAACTCTACTGCAAAATTCGAAGACATGCCCCATC 660
Qy CAGATCAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Db CAGATCAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Qy AAAAAAGCTGAGCAGCTCAGGAGTGTGAAGCGGTGCCCCCAACCATGAGCTGAGCCGT 780
Db AAAAAAGCTGAGCAGCTCAGGAGTGTGAAGCGGTGCCCCCAACCATGAGCTGAGCCGT 780
Qy GAATTCACAGGAGCAGATTCGCCCTCTCTAGTCAATTCATTCGAGTAGAGGGAACAGC 840
Db GAATTCACAGGAGCAGATTCGCCCTCTCTAGTCAATTCATTCGAGTAGAGGGAACAGC 840
Qy CATGCCAGTATGTAGAAGATCCCATCAGAGGAGCAGAGTGTGCTGTTACCTTATGAG 900
Db CATGCCAGTATGTAGAAGATCCCATCAGAGGAGCAGAGTGTGCTGTTACCTTATGAG 900
Qy CACCCCGAGTTGGCACTGAAATTCACGACAGTCTTGTACAATTCATGTGTAAACAGCAGT 960
Db CACCCCGAGTTGGCACTGAAATTCACGACAGTCTTGTACAATTCATGTGTAAACAGCAGT 960
Qy TGTGTTGAGGGGATGAACCGCGTCCAAATTTAAATCAATTTGTTACTCTGGAACACAGAT 1020
Db TGTGTTGAGGGGATGAACCGCGTCCAAATTTAAATCAATTTGTTACTCTGGAACACAGAT 1020
Qy GGCAAGTCTCTGGCCGACGCTGCTTTGAGGCCCGGATCTGTGCTTGCCTCCAGGAAGAGC 1080
Db GGCAAGTCTCTGGCCGACGCTGCTTTGAGGCCCGGATCTGTGCTTGCCTCCAGGAAGAGC 1080
Qy AGAAGCGCGATGAAGATAGCATTCAGAAAGCAGCAAGTTTCGGACAGTACAAAGACCGT 1140
Db AGAAGCGCGATGAAGATAGCATTCAGAAAGCAGCAAGTTTCGGACAGTACAAAGACCGT 1140
Qy GATGTACCAAGCGCCGTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
Db GATGTACCAAGCGCCGTTTCGTGAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
Qy AAACGAGATCCCAGATGATGAATCTGTTTATCTTACCAAGTGAAGGCCGCTGAGACTTAT 1260
Db AAACGAGATCCCAGATGATGAATCTGTTTATCTTACCAAGTGAAGGCCGCTGAGACTTAT 1260
Qy GAAATGCTTTGAAGATCAAGAGTCCCTGGAACTCATGAGTACCTTCTCTCAGCACACA 1320
Db GAAATGCTTTGAAGATCAAGAGTCCCTGGAACTCATGAGTACCTTCTCTCAGCACACA 1320
Qy ATTGAACCTGACGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
Db ATTGAACCTGACGCAACAGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1380
Qy CTTTCAGCCTGCTTTCAGGAAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAAACATCT 1440
Db CTTTCAGCCTGCTTTCAGGAAATGAGCTTGTGGAGCCCGGAGAGAACTCCAAAACATCT 1440
Qy GACGCTCTTTAGACATTCAGAGCCCCCAACCGATCAGTGTACCCATAGAGCCCTATC 1500
Db GACGCTCTTTAGACATTCAGAGCCCCCAACCGATCAGTGTACCCATAGAGCCCTATC 1500
Qy TCTATATTTTAAAGTGTGTTGTTTATTTCCATGTTATGTTGAGTGTGTTGTTGTTA 1560
Db TCTATATTTTAAAGTGTGTTGTTTATTTCCATGTTATGTTGAGTGTGTTGTTGTTA 1560

```
Qy 1561 TGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTTGAAGACACTTTTGGCTCAGAGA 1620
Db 1561 TGTGTGCGTGTGTATCTAGCCCTCATAAACAGGACTTTGAAGACACTTTTGGCTCAGAGA 1620
Qy 1621 CCCAACTGCTCAAGGGCAAAAGCCACTAGTGTGAGAGAACTCTTTTGAAGGACTCAAAACCT 1680
Db 1621 CCCAACTGCTCAAGGGCAAAAGCCACTAGTGTGAGAGAACTCTTTTGAAGGACTCAAAACCT 1680
Qy 1681 TTACAAGAAAGGATGTTTTCTGTCAGATTTTGTATCCTTAGACCGCCATTGCTGGGTGAG 1740
Db 1681 TTACAAGAAAGGATGTTTTCTGTCAGATTTTGTATCCTTAGACCGCCATTGCTGGGTGAG 1740
Qy 1741 GAACCACTGTGTTTCTGTCGAGCTTTCTGTGTTTCTCGGAGGGGCTCAGGTGGG 1800
Db 1741 GAACCACTGTGTTTCTGTCGAGCTTTCTGTGTTTCTCGGAGGGGCTCAGGTGGG 1800
Qy 1801 GAAAGGGGCATTAGATGTTTATTTGGAACCTTTTCTGTCCTCTCTGTTGTTTCTTAA 1860
Db 1801 GAAAGGGGCATTAGATGTTTATTTGGAACCTTTTCTGTCCTCTCTGTTGTTTCTTAA 1860
Qy 1861 AATTACAGGGAAGCTTTTGAGCAGGCTCTCAAACTTAAAGATGTCCTTTTAAAGAAAGGAG 1920
Db 1861 AATTACAGGGAAGCTTTTGAGCAGGCTCTCAAACTTAAAGATGTCCTTTTAAAGAAAGGAG 1920
Qy 1921 AAAAAAGTTGTTATTTGTCGTGCATAAGTGTAGGTGACTGAGAGACTCAGTCAGA 1980
Db 1921 AAAAAAGTTGTTATTTGTCGTGCATAAGTGTAGGTGACTGAGAGACTCAGTCAGA 1980
Qy 1981 CCCTTTTAAATGCTGCTCAATGTAATTAATTCGAAGTAGTAAAGGAGTCAAGTG 2040
Db 1981 CCCTTTTAAATGCTGCTCAATGTAATTAATTCGAAGTAGTAAAGGAGTCAAGTG 2040
Qy 2041 TACTGCTGGGAGGAGTGTATCAATACCAAAAGTAACTTTGTTGGTGGAGGTTT 2100
Db 2041 TACTGCTGGGAGGAGTGTATCAATACCAAAAGTAACTTTGTTGGTGGAGGTTT 2100
Qy 2101 TTTGTGAGAACTTGCATTATTTGTCCTCCCTCATGTGTAGGTAGAGAACTTTCTTAAT 2160
Db 2101 TTTGTGAGAACTTGCATTATTTGTCCTCCCTCATGTGTAGGTAGAGAACTTTCTTAAT 2160
Qy 2161 GCTGTGTACCTGCTGCGACTGTATGTTGGCATCTGTTATGCTAAAGTTTTCTTGTA 2220
Db 2161 GCTGTGTACCTGCTGCGACTGTATGTTGGCATCTGTTATGCTAAAGTTTTCTTGTA 2220
Qy 2221 CATGAAACCTTGGAGACCTACTACAAAGAACTGTTGTTGGCCCCCATAGCAGGTGAA 2280
Db 2221 CATGAAACCTTGGAGACCTACTACAAAGAACTGTTGTTGGCCCCCATAGCAGGTGAA 2280
Qy 2281 CTCATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCAGTAATATTTGCCCTTACGTAGT 2340
Db 2281 CTCATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCAGTAATATTTGCCCTTACGTAGT 2340
Qy 2341 TGTTTACCATATTTCAAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATT 2400
Db 2341 TGTTTACCATATTTCAAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAATCTGTGATT 2400
Qy 2401 AATTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACTACCAATAAAACAGCCATATTA 2460
Db 2401 AATTGCTTAATTAGAGCTTCTATCCCTCAAGCCTACTACCAATAAAACAGCCATATTA 2460
Qy 2461 CTGATCTGTTCAAGTCATTTAGCCAGGAGACTTTACGTTTGTAGTAAGTGAGATCCAAAGC 2520
Db 2461 CTGATCTGTTCAAGTCATTTAGCCAGGAGACTTTACGTTTGTAGTAAGTGAGATCCAAAGC 2520
Qy 2521 AGACGTGTTAAATCAGCACTCTCTGGACTGGAATTTAAAGATTTGAAAGGTTAGACTACTT 2580
Db 2521 AGACGTGTTAAATCAGCACTCTCTGGACTGGAATTTAAAGATTTGAAAGGTTAGACTACTT 2580
Qy 2581 TTCTTTTTTTTACTCAAAAGTTTAGAGAACTCTGTTTCTTTTCCATTTTAAACAATATT 2640
Db 2581 TTCTTTTTTTTACTCAAAAGTTTAGAGAACTCTGTTTCTTTTCCATTTTAAACAATATT 2640
```

```
Qy 2641 TTAAGATAATAGCATAAAGACTTTTAAAAATGTTTCTCCCTCCATCTTCCACACCCAGT 2700
Db 2641 TTAAGATAATAGCATAAAGACTTTTAAAAATGTTTCTCCCTCCATCTTCCACACCCAGT 2700
Qy 2701 CACCAGCACTGTATTTTCTGTGCACCAAGACAAATGATTTCTTGTTATTAGAGCTGTGCTT 2760
Db 2701 CACCAGCACTGTATTTTCTGTGCACCAAGACAAATGATTTCTTGTTATTAGAGCTGTGCTT 2760
Qy 2761 TTGTGGATGTGTGATTTTAAATTTTCAATAAACTTTTGCATCTTCTGTTTAAAGAAA 2816
Db 2761 TTGTGGATGTGTGATTTTAAATTTTCAATAAACTTTTGCATCTTCTGTTTAAAGAAA 2816

RESULT 13
US-10-393-567-65
; Sequence 65, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
; US-10-393-567-65

Query Match 100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCTGTATATCAAGACAGTTGAAGGAAATGAAATTTTGAAACTTCACGGTGTGCCACCT 60
Db 1 TCCTGTATATCAAGACAGTTGAAGGAAATGAAATTTTGAAACTTCACGGTGTGCCACCT 60
Qy 61 ACAGTACTGCCCTGACCTTTACATCCAGCGCTTCGTAGAAACCCAGCTCATTTCTCTGG 120
Db 61 ACAGTACTGCCCTGACCTTTACATCCAGCGCTTCGTAGAAACCCAGCTCATTTCTCTGG 120
Qy 121 AAGAAAGTTTATACCGATCGCCAGAGCACAGACAAATGAATTCCTCAGT 180
Db 121 AAGAAAGTTTATACCGATCGCCAGAGCACAGACAAATGAATTCCTCAGT 180
Qy 181 CCAGAGCTTTCCAGCATATCTGGGATTTTCTGGAAACAGCTATATGTTTCAGTTTCAGCCC 240
Db 181 CCAGAGCTTTCCAGCATATCTGGGATTTTCTGGAAACAGCTATATGTTTCAGTTTCAGCCC 240
Qy 241 ATTGACTTGAACCTTTGTGGATGAACCAATCAGAGATGGTGGCAAAACAAGATTGAGATT 300
Db 241 ATTGACTTGAACCTTTGTGGATGAACCAATCAGAGATGGTGGCAAAACAAGATTGAGATT 300
Qy 301 AGCATGGATGTATCCGATCGAGGACTCGGACCTGAGTCACCCCATGTGCGCCACAGTAC 360
Db 301 AGCATGGATGTATCCGATCGAGGACTCGGACCTGAGTCACCCCATGTGCGCCACAGTAC 360
Qy 361 ACGAACCTGGGGCTCTCTGAACAGCATGGACAGCAATTCAGAACGGCTCTCTCGTCCACC 420
Db 361 ACGAACCTGGGGCTCTCTGAACAGCATGGACAGCAATTCAGAACGGCTCTCTCGTCCACC 420
Qy 421 AGTCCCTATAACACAGACCAAGCGCAGAACAGCGTCAAGCGCGCTCGCCCTACGCAAG 480
Db 421 AGTCCCTATAACACAGACCAAGCGCAGAACAGCGTCAAGCGCGCTCGCCCTACGCAAG 480
Qy 481 CCAGCTCCACCTTTCAGTGTCTCTCCATCACCAGGCTATCCCTCCAAACAGGACTAC 540
Db 481 CCAGCTCCACCTTTCAGTGTCTCTCCATCACCAGGCTATCCCTCCAAACAGGACTAC 540
```

Qy	541	CCAGGCCGCGACAGATTTT	CGA	CGTGTCTCTTCCAGCAGT	CGAGCACCGCCAAAGT	TCGGCCACC	600
Db	541	CCAGGCCGCGACAGATTTT	CGA	CGTGTCTCTTCCAGCAGT	CGAGCACCGCCAAAGT	TCGGCCACC	600
Qy	601	TGGACGTATTCACAC	TGAAGAAA	CTCTACTG	TGCCAAAT	TTGCAAAAGACATGCCCCATC	660
Db	601	TGGACGTATTTCCACT	TGAATCTGA	AGAAATCT	TATCTGCCAAAT	TTGCAAAAGACATGCCCCATC	660
Qy	661	CAGATCAAGAGTGAT	GACCCCCACCT	CCTCAGGAGAGCT	GTATTC	CGCGCCATGCCCTGTCTAC	720
Db	661	CAGATCAAGAGTGAT	GACCCCCACCT	CCTCAGGAGAGCT	GTATTC	CGCGCCATGCCCTGTCTAC	720
Qy	721	AAAAAAGCTGAGCAG	CGTCA	CGGAGTG	TGTAAGCGGTC	CCCAACCATAGAGCTGAGCGGT	780
Db	721	AAAAAAGCTGAGCAG	CGTCA	CGGAGTG	TGTAAGCGGTC	CCCAACCATAGAGCTGAGCGGT	780
Qy	781	GAAATTC	CAACGAGGACAGAT	TGCCCCCT	CCTAGTCA	TTTGTATTCAGATAGAGGGGAA	840
Db	781	GAAATTC	CAACGAGGACAGAT	TGCCCCCT	CCTAGTCA	TTTGTATTCAGATAGAGGGGAA	840
Qy	841	CATGCCCATGATGT	AGAAAGATCCCAT	CACAGGAA	GACAGAGTG	TGCTTATTCAG	900
Db	841	CATGCCCATGATGT	AGAAAGATCCCAT	CACAGGAA	GACAGAGTG	TGCTTATTCAG	900
Qy	901	CCACCCAGGTTGG	CAC	TGAATTC	ACGACAGTCT	TGTGTA	960
Db	901	CCACCCAGGTTGG	CAC	TGAATTC	ACGACAGTCT	TGTGTA	960
Qy	961	TGTGTTGAGGGAT	GAACCGCGCT	CCAAATTT	TAATCAT	TGTTACTCTGGGAA	1020
Db	961	TGTGTTGAGGGAT	GAACCGCGCT	CCAAATTT	TAATCAT	TGTTACTCTGGGAA	1020
Qy	1021	GGGCAAGTCTCT	GGGCGCAGCGT	TGTTG	AGGCGCGGATCT	GTGCTTGCCAGGAA	1080
Db	1021	GGGCAAGTCTCT	GGGCGCAGCGT	TGTTG	AGGCGCGGATCT	GTGCTTGCCAGGAA	1080
Qy	1081	AGGAAGGCGGAT	GAAGATAG	CAT	CAGAAAGCAG	CAAGTTTCGGACAGT	1140
Db	1081	AGGAAGGCGGAT	GAAGATAG	CAT	CAGAAAGCAG	CAAGTTTCGGACAGT	1140
Qy	1141	GATGGTAG	CGACCGCCGTTT	CGTCAG	AACACAT	GGTATCCAGATG	1200
Db	1141	GATGGTAG	CGACCGCCGTTT	CGTCAG	AACACAT	GGTATCCAGATG	1200
Qy	1201	AAACGAAGAT	CCCCAGATG	ATACTG	TATTA	TACTTAC	1260
Db	1201	AAACGAAGAT	CCCCAGATG	ATACTG	TATTA	TACTTAC	1260
Qy	1261	GAAATGCTGTT	GAAGATCA	AAAGAGT	CCCTGG	AACTCAT	1320
Db	1261	GAAATGCTGTT	GAAGATCA	AAAGAGT	CCCTGG	AACTCAT	1320
Qy	1321	ATTGAAAGCT	CAGGCAACG	ACACG	CAGCAGC	ACCAAGCACTT	1380
Db	1321	ATTGAAAGCT	CAGGCAACG	ACACG	CAGCAGC	ACCAAGCACTT	1380
Qy	1381	CTTTGAGC	CTGCTT	CAGGAATG	AGCTTGT	GAGGCCG	1440
Db	1381	CTTTGAGC	CTGCTT	CAGGAATG	AGCTTGT	GAGGCCG	1440
Qy	1441	GACGTCTTT	TAGACATTC	CAAGCC	CCCCAAAC	CGATG	1500
Db	1441	GACGTCTTT	TAGACATTC	CAAGCC	CCCCAAAC	CGATG	1500
Qy	1501	TCTATATTT	TAAGTGTGTG	TGTTG	TATTTT	CACTGT	1560
Db	1501	TCTATATTT	TAAGTGTGTG	TGTTG	TATTTT	CACTGT	1560
Qy	1561	TGTGTG	CGGTGTG	TATCT	AGCCCT	CTATAA	1620
Db	1561	TGTGTG	CGGTGTG	TATCT	AGCCCT	CTATAA	1620
Qy	1621	CCCAACT	GTCTCA	AAAGGCA	CAAGGCACT	GTAGAG	1680

Db	1621	CCCAACTGCTCAAAAGGCACAAGGCCACTAGTGAGAAATCTTTTGAAGGGCACTCAAACTT	1681
Qy	1681	TTACAAGAAAGGATGTTTTCTGTCAGATTTTGTGATCCTTAGACCGGCATTTGGTGGGTGAG	1740
Db	1681	TTACAAGAAAGGATGTTTTCTGTCAGATTTTGTGATCCTTAGACCGGCATTTGGTGGGTGAG	1740
Qy	1741	GAACCACTGTTTGTCTGTGAGCTTTCTGTGTTTCTCTGGGAGGAGGGGTGAGTGGG	1800
Db	1741	GAACCACTGTTTGTCTGTGAGCTTTCTGTGTTTCTCTGGGAGGAGGGGTGAGTGGG	1800
Qy	1801	GAAGGGGCATTAAGATGTTTTATTTGGAAACCTTTTCTGTCTCTCTCTGTGTTTTTCTAA	1860
Db	1801	GAAGGGGCATTAAGATGTTTTATTTGGAAACCTTTTCTGTCTCTCTCTGTGTTTTTCTAA	1860
Qy	1861	AATTCACAGGAAGCTTTTTCAGCAGGTCTCAAACTTTAAGATGTCCTTTTTAAGAAAAAGGAG	1920
Db	1861	AATTCACAGGAAGCTTTTTCAGCAGGTCTCAAACTTTAAGATGTCCTTTTTAAGAAAAAGGAG	1920
Qy	1921	AAAAAAGTCTTATTTGTCTGTGCAATAAGTAAGTTGTAGTGTACTGAGAGACTCAGTCAGA	1980
Db	1921	AAAAAAGTCTTATTTGTCTGTGCAATAAGTAAGTTGTAGTGTACTGAGAGACTCAGTCAGA	1980
Qy	1981	CCCTTTTAATGCTGGTCACTGTAATAATATTTGCAAGTAGTAAGNAACGAAGGTGTCAGTG	2040
Db	1981	CCCTTTTAATGCTGGTCACTGTAATAATATTTGCAAGTAGTAAGNAACGAAGGTGTCAGTG	2040
Qy	2041	TACTGCTGGCAGCAGGTGCATCATTTACCAAAAGTAATCAACTTTCTGGGTGAGAGTTTC	2100
Db	2041	TACTGCTGGCAGCAGGTGCATCATTTACCAAAAGTAATCAACTTTCTGGGTGAGAGTTTC	2100
Qy	2101	TTTTGTGAGAACTTTGCATTATTTGTGTCCTCCCTCATGTGTAGGTAGAACATTTCTTAAT	2160
Db	2101	TTTTGTGAGAACTTTGCATTATTTGTGTCCTCCCTCATGTGTAGGTAGAACATTTCTTAAT	2160
Qy	2161	GCTGTGTACTGCTGCTGCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCTTGTA	2220
Db	2161	GCTGTGTACTGCTGCTGCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCTTGTA	2220
Qy	2221	CATGAAACCCCTGGAAGACCTACTACAAAAAAACCTGTTGTTGGCCCCCCTACAGAGTGAA	2280
Db	2221	CATGAAACCCCTGGAAGACCTACTACAAAAAAACCTGTTGTTGGCCCCCCTACAGAGTGAA	2280
Qy	2281	CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTTGCCCTTACGTAGT	2340
Db	2281	CTCATTTTGTGCTTTTAATAGAAAGACAAATCCACCCCAGTAATATTTGCCCTTACGTAGT	2340
Qy	2341	TGTTTACCATTATTTCAAGCTCAAAATAGNAATTTGAAGCCCTCTCAAAAAATCTGTGATT	2400
Db	2341	TGTTTACCATTATTTCAAGCTCAAAATAGNAATTTGAAGCCCTCTCAAAAAATCTGTGATT	2400
Qy	2401	AATTTGCTTAATTTAGAGCTTCTATCCTCAAGCCTACCTACCATAAAACAGGCCATATTA	2460
Db	2401	AATTTGCTTAATTTAGAGCTTCTATCCTCAAGCCTACCTACCATAAAACAGGCCATATTA	2460
Qy	2461	CTGATCTGTTTACGTGCATTTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAGC	2520
Db	2461	CTGATCTGTTTACGTGCATTTAGCCAGGAGACTTACGTTTTGAGTAAGTGAGATCCAAGC	2520
Qy	2521	AGAGGTGTTAAATCAGCACTCTCTGACCTGGAAATTTAAAGATTGAAGGGTAGACTACTT	2580
Db	2521	AGAGGTGTTAAATCAGCACTCTCTGACCTGGAAATTTAAAGATTGAAGGGTAGACTACTT	2580
Qy	2581	TTCTTTTTTTTACTCAAAAGTTTAGAAGATCTCTGTTTTCTTCCATTTTTAAAAACATATT	2640
Db	2581	TTCTTTTTTTTACTCAAAAGTTTAGAAGATCTCTGTTTTCTTCCATTTTTAAAAACATATT	2640
Qy	2641	TTAAGATAATPAGCATAAAGACTTTAAAAATGTTTCTCCCTCCATCTTCCACACCCAGT	2700
Db	2641	TTAAGATAATPAGCATAAAGACTTTAAAAATGTTTCTCCCTCCATCTTCCACACCCAGT	2700
Qy	2701	CACGAGCACTGTAATTTTCTGTACCAAGACAATGATTTCTTGTTATTGAGGCTGTGCTT	2760

Db	2701 CACCAGCACGTGATTTTCTGTGCCAAGACAATGATTCTTGTTATTGAGCGCTGGTCGTT	2760
Qy	2761 TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTTGCATCTTGGTTTTAAAAGAAA	2816
Db	2761 TTGTGGATGTGTGATTTTAATTTTCAATAAACTTTTGCATCTTGGTTTTAAAAGAAA	2816

RESULT 14

```

US-10-394-087-26
; Sequence 26, Application US/10394087
; Publication No. US20030194734A1
; GENERAL INFORMATION:
; APPLICANT: Jatkeo, Tim
; TITLE OF INVENTION: SELECTION OF MARKERS
; FILE REFERENCE: CDS 265 US NP
; CURRENT APPLICATION NUMBER: US/10/394,087
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,790
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-394-087-26

```

Query Match	100.0%;	Score 2816;	DB 16;	Length 2816;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2816;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TCGTTGATATCAAAGACAGCTTGAAGGAAATGAATTTTGAACCTTCACGGTGTGCCACCCT	60	
DB	1	TCGTTGATATCAAAGACAGCTTGAAGGAAATGAATTTTGAACCTTCACGGTGTGCCACCCT	60	
QY	61	ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCAGCTCATTTCTCTTGG	120	
DB	61	ACAGTACTGCCCTGACCCCTTACATCCAGCGTTTCGTAGAAACCAGCTCATTTCTCTTGG	120	
QY	121	AAAGAAAGTTATTACCGATCCACATGTCCTCAGAGCACACAGACAAATGAATTCCTCAGT	180	
DB	121	AAAGAAAGTTATTACCGATCCACATGTCCTCAGAGCACACAGACAAATGAATTCCTCAGT	180	
QY	181	CCAGAGGTTTTCCAGCATATCTGGGATTTCTCGAACAGCGCTATATGTTTCAGTTTCAGCCC	240	
DB	181	CCAGAGGTTTTCCAGCATATCTGGGATTTCTCGAACAGCGCTATATGTTTCAGTTTCAGCCC	240	
QY	241	ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGGTGCACAAACAAAGATTGAGATT	300	
DB	241	ATTGACTTGAACCTTTGTGGATGAACCATCAGAAGATGGTGCACAAACAAAGATTGAGATT	300	
QY	301	AGCATGGACTGTATCCGCATGCAAGGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC	360	
DB	301	AGCATGGACTGTATCCGCATGCAAGGACTCGGACCTGAGTGACCCCATGTGGCCACAGTAC	360	
QY	361	ACGAACTGGGGCTCCTTGAACACAGCATGGACACAGATTCAGAACGGCTCTCGTCCACC	420	
DB	361	ACGAACTGGGGCTCCTTGAACACAGCATGGACACAGATTCAGAACGGCTCTCGTCCACC	420	
QY	421	AGTCCCTATAACACAGACCAACCGCGAGAACAGCGGTCAACGGCGCCCTCGCCCTACGCACAG	480	
DB	421	AGTCCCTATAACACAGACCAACCGCGAGAACAGCGGTCAACGGCGCCCTCGCCCTACGCACAG	480	
QY	481	CCGAGCTCCACCTTCGATGCTCTCTCCATACCCGCCATCCCTCTCGAACCCGACTAC	540	
DB	481	CCGAGCTCCACCTTCGATGCTCTCTCCATACCCGCCATCCCTCTCGAACCCGACTAC	540	
QY	541	CCAGGCCCGCACAGTTTCGACAGTGTCTTCCAGCAGTCGAGACCGCCAAAGTCGGCCACC	600	
DB	541	CCAGGCCCGCACAGTTTCGACAGTGTCTTCCAGCAGTCGAGACCGCCAAAGTCGGCCACC	600	
QY	601	TGGACGTATTTCACACTGAAAGAAACTCTACTGCGAAATTCGAAAGACATGCCCCATC	660	


```
QY 1741 GAACCACTGTTGTTCTGTGAGCTTTCTGTGTTCTCTGGGAGGAGGGGTCAAGTGG 1800
Db 1741 GAACCACTGTTGTTGTTGAGCTTTCTGTGTTCTCTGGGAGGAGGGGTCAAGTGG 1800
QY 1801 GAAAGGGCATTAAGATGTTTATTTGGAACCCCTTTCTGCTTCTGTTGTTTCTTAA 1860
Db 1801 GAAAGGGCATTAAGATGTTTATTTGGAACCCCTTTCTGCTTCTGTTGTTTCTTAA 1860
QY 1861 AATTCAAGGGAAGCTTTTGAGCAGGTCTCAAACTTAAGATGTTTCTTTTAAAGAAAGGAG 1920
Db 1861 AATTCAAGGGAAGCTTTTGAGCAGGTCTCAAACTTAAGATGTTTCTTTTAAAGAAAGGAG 1920
QY 1921 AAAAAAGTTGTTATTCGTGTGCATTAAGTAAGTTGAGTGAAGTGAAGTGAAGTGAAGTGA 1980
Db 1921 AAAAAAGTTGTTATTCGTGTGCATTAAGTAAGTTGAGTGAAGTGAAGTGAAGTGAAGTGA 1980
QY 1981 CCTTTTAAATGCTGTCATGTAATAATATTTGCAAGTAGTAAGAAAGTGAAGTGAAGTGA 2040
Db 1981 CCTTTTAAATGCTGTCATGTAATAATATTTGCAAGTAGTAAGAAAGTGAAGTGAAGTGA 2040
QY 2041 TACTGCTGGCAGCAGGTGATCATTTACCAAAAGTAATCAACTTTGTGGGTGGAGAGTTC 2100
Db 2041 TACTGCTGGCAGCAGGTGATCATTTACCAAAAGTAATCAACTTTGTGGGTGGAGAGTTC 2100
QY 2101 TTTGTGAGAACTTGCAATTAATTTGTGTCCTCCCTCATGTGTAGTGAAGACATTTCTTAAT 2160
Db 2101 TTTGTGAGAACTTGCAATTAATTTGTGTCCTCCCTCATGTGTAGTGAAGACATTTCTTAAT 2160
QY 2161 GCTGTGTACCTGCTCGCCACTGATGTTGGCATCTGTTATGCTAAAGTTTTCTTGTA 2220
Db 2161 GCTGTGTACCTGCTCGCCACTGATGTTGGCATCTGTTATGCTAAAGTTTTCTTGTA 2220
QY 2221 CATGAAACCTGGAAGACCTACTACAAAAAACTGTTGTTGGCCCCCCTACAGAGTGAA 2280
Db 2221 CATGAAACCTGGAAGACCTACTACAAAAAACTGTTGTTGGCCCCCCTACAGAGTGAA 2280
QY 2281 CTCATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCCAAGTAATATGTCCTTACGTAGT 2340
Db 2281 CTCATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCCAAGTAATATGTCCTTACGTAGT 2340
QY 2341 TGTTTACCAATTAATCAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAAATCTGTGATT 2400
Db 2341 TGTTTACCAATTAATCAAGCTCAAAATAGAAATTTGAAGCCCTCTCAAAAAATCTGTGATT 2400
QY 2401 AATTGCTTAAATTAGAGCTTTATCCCTCAAGCCTACCTACCAATTAACCAAGCCATATTA 2460
Db 2401 AATTGCTTAAATTAGAGCTTTATCCCTCAAGCCTACCTACCAATTAACCAAGCCATATTA 2460
QY 2461 CTGATACCTGTTAGTGCAATTTAGCAGGAGACTTACGTTTGTAGTAAGTGAGATCCAGC 2520
Db 2461 CTGATACCTGTTAGTGCAATTTAGCAGGAGACTTACGTTTGTAGTAAGTGAGATCCAGC 2520
QY 2521 AGACGTGTTTAAATCAGCACTCTCGACTGGAAATTTAAAGATTTGAAGGGTGAAGTACTTT 2580
Db 2521 AGACGTGTTTAAATCAGCACTCTCGACTGGAAATTTAAAGATTTGAAGGGTGAAGTACTTT 2580
QY 2581 TTCCTTTTTTTTACTCAAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTTAAAAACATATT 2640
Db 2581 TTCCTTTTTTTTACTCAAAAAGTTTAGAGAATCTCTGTTTCTTTCCATTTTAAAAACATATT 2640
QY 2641 TTAAGATAATAGCATAAAGACTTTTAAATAATGTTTCCCTCCCTCATCTTCCACACCCAGT 2700
Db 2641 TTAAGATAATAGCATAAAGACTTTTAAATAATGTTTCCCTCCCTCATCTTCCACACCCAGT 2700
QY 2701 CACCAGCACTGATTTTCTGTCCACCAAGACAATGATTTCTGTTATGAGGCTGTTGCTT 2760
Db 2701 CACCAGCACTGATTTTCTGTCCACCAAGACAATGATTTCTGTTATGAGGCTGTTGCTT 2760
QY 2761 TTGTGATGTTGATTTTAAATTTTCAATAAAATTTTGCATCTTTGGTTTAAAAAGAAA 2816
Db 2761 TTGTGATGTTGATTTTAAATTTTCAATAAAATTTTGCATCTTTGGTTTAAAAAGAAA 2816
```

```
RESULT 15
US-10-394-087-27
; Sequence 27, Application US/10394087
; Publication No. US20030194734A1
; GENERAL INFORMATION:
; APPLICANT: Jatkoe, Tim
; TITLE OF INVENTION: SELECTION OF MARKERS
; FILE REFERENCE: CDS 265 US NP
; CURRENT APPLICATION NUMBER: US/10/394,087
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,790
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: human
US-10-394-087-27
```

```
Query Match 100.0%; Score 2816; DB 16; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTTGATATCAAGACAGAGTTGAAGGAAATGAAATTTTCAAACTTCAACGGTGTGCCACCT 60
Db 1 TCGTTGATATCAAGACAGAGTTGAAGGAAATGAAATTTTCAAACTTCAACGGTGTGCCACCT 60
QY 61 ACAGTACTGCCCTGACCTTACATCCAGGTTTCTAGAAACCCAGCTCATTTCTTGG 120
Db 61 ACAGTACTGCCCTGACCTTACATCCAGGTTTCTAGAAACCCAGCTCATTTCTTGG 120
QY 121 AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGACAAATTCCTCAGT 180
Db 121 AAAGAAAGTTATTACCGATCCACCATGTCCAGAGCACACAGACAAATTCCTCAGT 180
QY 181 CCAGAGGTTTCCAGCATATCTGGGATTTCTGGAAACAGCCTATATGTTTCAGTTCAGCCC 240
Db 181 CCAGAGGTTTCCAGCATATCTGGGATTTCTGGAAACAGCCTATATGTTTCAGTTCAGCCC 240
QY 241 ATTGACTTGAATTTTGTGGATGAACCATCAGAAAGATGTTGCGACAAAACAAGATTGAGATT 300
Db 241 ATTGACTTGAATTTTGTGGATGAACCATCAGAAAGATGTTGCGACAAAACAAGATTGAGATT 300
QY 301 AGCATGGACTGTATCCGCATCGAGACTCGGACCTCGAGTGCACCCATGTGGCCACAGTAC 360
Db 301 AGCATGGACTGTATCCGCATCGAGACTCGGACCTCGAGTGCACCCATGTGGCCACAGTAC 360
QY 361 ACGAACCTGGGGCTCTCTGAAACAGCATGGACAGCAGATTTCAGAACGGCTCCTCGTCCACC 420
Db 361 ACGAACCTGGGGCTCTCTGAAACAGCATGGACAGCAGATTTCAGAACGGCTCCTCGTCCACC 420
QY 421 AGTCCCTATAACACAGACACCGCGCAGAACAGCTGCAGGCGCCCTCGGCCCTACGACAG 480
Db 421 AGTCCCTATAACACAGACACCGCGCAGAACAGCTGCAGGCGCCCTCGGCCCTACGACAG 480
QY 481 CCCAGCTCCACTTCGATGCTCTCTCATCACCGCCCATCCCTCCAAACCCGACTAC 540
Db 481 CCCAGCTCCACTTCGATGCTCTCTCATCACCGCCCATCCCTCCAAACCCGACTAC 540
QY 541 CCAGCGCCGACAGTTTTCGAGCTGTTCTTCCAGCAGTCCAGCACCGCCCAAGTCGGCCACC 600
Db 541 CCAGCGCCGACAGTTTTCGAGCTGTTCTTCCAGCAGTCCAGCACCGCCCAAGTCGGCCACC 600
QY 601 TGGAGCTATTCCATGAACTGAAGAACTCTACTGCCAAATTTGCAAGACATGCCCCATC 660
Db 601 TGGAGCTATTCCATGAACTGAAGAACTCTACTGCCAAATTTGCAAGACATGCCCCATC 660
QY 661 CAGATCAAGGTGATGACCCCTCTCCTCAGGAGCTGTTATCCGCGCATGCTGTCTAC 720
Db 661 CAGATCAAGGTGATGACCCCTCTCCTCAGGAGCTGTTATCCGCGCATGCTGTCTAC 720
```


Qy 721 AAAAAAGCTGAGCAGCTCACGAGGTGGTGAAGCGGTGCCCCAACCCATGAGCTGAGCGGT 780
Db 721 AAAAAAGCTGAGCAGCTCACGAGGTGGTGAAGCGGTGCCCCAACCCATGAGCTGAGCGGT 780
Qy 781 GAATTCACGAGGACAGATTGGCCCTCCTAGTCAATTTGATTCGAGTAGGGGAAACAGC 840
Db 781 GAATTCACGAGGACAGATTGGCCCTCCTAGTCAATTTGATTCGAGTAGGGGAAACAGC 840
Qy 841 CATGCCAGTATGTAGAGATCCCACACAGAAAGACAGAGTGTGCTGGTACCTTATGAG 900
Db 841 CATGCCAGTATGTAGAGATCCCACACAGAAAGACAGAGTGTGCTGGTACCTTATGAG 900
Qy 901 CCACCCAGGTGGCAGCTGAATTCACGACAGTCTTTGACAAATTCATGTTGTAACAGAGT 960
Db 901 CCACCCAGGTGGCAGCTGAATTCACGACAGTCTTTGACAAATTCATGTTGTAACAGAGT 960
Qy 961 TGTGTTGAGGGATGAACCGCGTCCAAATTTAATCATTTGTTACTCTGGAAACACAGAGAT 1020
Db 961 TGTGTTGAGGGATGAACCGCGTCCAAATTTAATCATTTGTTACTCTGGAAACACAGAGAT 1020
Qy 1021 GGGCAAGTCTTGGGCCGACGCTGCTTTGAGGCCCGGATCTGTGCTTGGCCACGAGAGAC 1080
Db 1021 GGGCAAGTCTTGGGCCGACGCTGCTTTGAGGCCCGGATCTGTGCTTGGCCACGAGAGAC 1080
Qy 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTGGGACAGTACAAAGAACCGT 1140
Db 1081 AGGAAGCGGATGAAGATAGCATCAGAAAGCAGCAAGTTTGGGACAGTACAAAGAACCGT 1140
Qy 1141 GATGGTACGAGCGCCCGTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
Db 1141 GATGGTACGAGCGCCCGTTCGTCAGAACACACATGGTATCCAGATGACATCCATCAAG 1200
Qy 1201 AAACGAAAGTCCCGAGATGATGAATCTTACTTACGAGTGGGGCCGTGAGACTTAT 1260
Db 1201 AAACGAAAGTCCCGAGATGATGAATCTTACTTACGAGTGGGGCCGTGAGACTTAT 1260
Qy 1261 GAAATGCTGTGAAGATCAAAGAGTCCCTGAACTCATGACAGTACCTTCTCAGCACACA 1320
Db 1261 GAAATGCTGTGAAGATCAAAGAGTCCCTGAACTCATGACAGTACCTTCTCAGCACACA 1320
Qy 1321 ATTGAACGTTACGGCAACAGCAACAGCAGCAGCAGCAGTACTTTCAGAACATCTC 1380
Db 1321 ATTGAACGTTACGGCAACAGCAACAGCAGCAGCAGCAGTACTTTCAGAACATCTC 1380
Qy 1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGAGCCCGGAGAGAACTCCAAAACAACTCT 1440
Db 1381 CTTTCAGCCTGCTTCAGGAATGAGCTTGTGAGCCCGGAGAGAACTCCAAAACAACTCT 1440
Qy 1441 GAGCTCTTCTTTAGACATTCAGCCGCCAAACCGATCAGTGTAACCATAGAGCCCTATC 1500
Db 1441 GAGCTCTTCTTTAGACATTCAGCCGCCAAACCGATCAGTGTAACCATAGAGCCCTATC 1500
Qy 1501 TCTATATTTAAGTGTGTGTGTATTTCCATGTGTATATGTCAGTGTGTGTGTGTA 1560
Db 1501 TCTATATTTAAGTGTGTGTGTATTTCCATGTGTATATGTCAGTGTGTGTGTGTA 1560
Qy 1561 TGTGTGTGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620
Db 1561 TGTGTGTGTGTGTATCTAGCCCTCATAAACAGGACTTGAAGACACTTTGGCTCAGAGA 1620
Qy 1621 CCCAACTGCTCAAGGACAAAGCCACTAGTGAGAGAACTTTTGAAGGAGACTCAAACT 1680
Db 1621 CCCAACTGCTCAAGGACAAAGCCACTAGTGAGAGAACTTTTGAAGGAGACTCAAACT 1680
Qy 1681 TTACAAGAAAGGATGTTTTCTGAGATTTTGTATCTTACACCGGCCATTTGGTGGTGAG 1740
Db 1681 TTACAAGAAAGGATGTTTTCTGAGATTTTGTATCTTACACCGGCCATTTGGTGGTGAG 1740
Qy 1741 GAACCACTGTGTTGTCTGTGAGCTTCTGTGTTTCTCTGGAGGGAGGGTCAAGTGGG 1800
Db 1741 GAACCACTGTGTTGTCTGTGAGCTTCTGTGTTTCTCTGGAGGGAGGGTCAAGTGGG 1800
Qy 1801 GAAAGGGGCATTAAGATGTTTATTTGGAACCCCTTTCTGCTCTTCTGTTTCTTCTAA 1860

Db 1801 GAAAGGGGCATTAAGATGTTTATTTGGAACCCCTTTCTGCTCTTCTGTTCTTCTAA 1860
Qy 1861 AATTCACAGGGAAGCTTTTCAGCAGAGTCTCAAACTTAAGATGCTCTTTTAAAGAAAGAG 1920
Db 1861 AATTCACAGGGAAGCTTTTCAGCAGAGTCTCAAACTTAAGATGCTCTTTTAAAGAAAGAG 1920
Qy 1921 AAAAAAGTTGTTATTTGTCTGTGCATTAAGTAAGTTGTAGGTGACTGAGAGACTCAAGT 1980
Db 1921 AAAAAAGTTGTTATTTGTCTGTGCATTAAGTAAGTTGTAGGTGACTGAGAGACTCAAGT 1980
Qy 1981 CCCTTTTAATGCTGCTCATGTAATAATTTGCAAGTAGTAAGTAAGTAAGTAAGTAAGT 2040
Db 1981 CCCTTTTAATGCTGCTCATGTAATAATTTGCAAGTAGTAAGTAAGTAAGTAAGT 2040
Qy 2041 TACTGCTGGGACGAGGTGATCATTTACCAAAAAGTAAATCAACTTTTGGTGGGAGAGTTC 2100
Db 2041 TACTGCTGGGACGAGGTGATCATTTACCAAAAAGTAAATCAACTTTTGGTGGGAGAGTTC 2100
Qy 2101 TTTGTGAGAACTTGCAATTTATTTGTCTCTCCCTCATGTGTAGGTAGAAACATTTCTTAAT 2160
Db 2101 TTTGTGAGAACTTGCAATTTATTTGTCTCTCCCTCATGTGTAGGTAGAAACATTTCTTAAT 2160
Qy 2161 GCTGTGTACTGCTCTGCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCTTGTA 2220
Db 2161 GCTGTGTACTGCTCTGCCACTGTATGTTGGCATCTGTTATGCTAAAGTTTTTCTTGTA 2220
Qy 2221 CATGAACCCCTGGAAGACCTACTACAAAAAACTGTTGTTTGGCCCCCATAGCAGGTGAA 2280
Db 2221 CATGAACCCCTGGAAGACCTACTACAAAAAACTGTTGTTTGGCCCCCATAGCAGGTGAA 2280
Qy 2281 CTCATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCCAGTAATATTTGCCCTTACGTAGT 2340
Db 2281 CTCATTTTGTGCTTTTAAATAGAAAGACAAATCCACCCCAGTAATATTTGCCCTTACGTAGT 2340
Qy 2341 TGTTTACCATTTTCAAGCTCAAAATAGAAATTTGAAGCCCTCTCAGAAAATCTGTGATT 2400
Db 2341 TGTTTACCATTTTCAAGCTCAAAATAGAAATTTGAAGCCCTCTCAGAAAATCTGTGATT 2400
Qy 2401 AATTTGCTTAATTAGAGCTTCTATCCTCAAGCTTACTACCAATAAAACAGCCATATTA 2460
Db 2401 AATTTGCTTAATTAGAGCTTCTATCCTCAAGCTTACTACCAATAAAACAGCCATATTA 2460
Qy 2461 CTGATACTGTTCAAGTCAATTTAGCCAGGAGACTTACGTTTGGAGTAAGTGAGATCCAAGC 2520
Db 2461 CTGATACTGTTCAAGTCAATTTAGCCAGGAGACTTACGTTTGGAGTAAGTGAGATCCAAGC 2520
Qy 2521 AGACGTGTTTAAATCAGCCTCCTGGACTGGAATTTAAAGATTGAAGGGGTAGACTACTT 2580
Db 2521 AGACGTGTTTAAATCAGCCTCCTGGACTGGAATTTAAAGATTGAAGGGGTAGACTACTT 2580
Qy 2581 TTCTTTTTTTTACTCAAAAGTTTAGAGAACTCTGTTTCTTCCATTTTAAAAACATATT 2640
Db 2581 TTCTTTTTTTTACTCAAAAGTTTAGAGAACTCTGTTTCTTCCATTTTAAAAACATATT 2640
Qy 2641 TTAAAGATAATAGCATAAAGAGTTTAAAAATGTTTCCCTCCCTCCATCTTCCACACCCAGT 2700
Db 2641 TTAAAGATAATAGCATAAAGAGTTTAAAAATGTTTCCCTCCCTCCATCTTCCACACCCAGT 2700
Qy 2701 CACACGACTGTATTTTCTGTGACCAAGACAAATGATTTCTTGTATTGAGGCTGTGCTT 2760
Db 2701 CACACGACTGTATTTTCTGTGACCAAGACAAATGATTTCTTGTATTGAGGCTGTGCTT 2760
Qy 2761 TTGTGGATGTGATTTTAAATTTTCAATAAATTTTGCATCTTGGTTTAAAAAGAAA 2816
Db 2761 TTGTGGATGTGATTTTAAATTTTCAATAAATTTTGCATCTTGGTTTAAAAAGAAA 2816

Search completed: October 3, 2005, 14:01:42

Job time : 2192 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 3, 2005, 06:01:58 ; Search time 247 Seconds
(without alignments)
2967.822 Million cell updates/sec

Title: US-09-670-568C-1

Perfect score: 2383

Sequence: 1 MSQSTQTNBFLSPVQHIW.....PKQSDVFFRRSKPPNRSVYP 448

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model -DSV=xlh
-Q-/cgn2_1/USPTO.spool/US09670568/runat_03102005_070150_24303/app_query.fasta_1.647
-DB-Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09670568@cgn 1.1.177 @runat_03102005_070150_24303 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCKS=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued Patents NA.*
- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2383	100.0	2810	4	US-09-949-016-5447
2	2383	100.0	2816	3	Sequence 5447, App
3	2383	100.0	2816	4	Sequence 333, App
4	2383	100.0	2816	4	US-09-542-615A-333
5	2383	100.0	2816	4	US-09-606-421B-333
6	2185	91.7	1551	3	US-09-630-940B-333
7	2185	91.7	1551	4	Sequence 337, App
8	2185	91.7	1551	4	US-09-542-615A-337
9	2185	91.7	1551	4	US-09-606-421B-337
10	2185	91.7	2270	3	US-09-630-940B-337
11	2185	91.7	2270	4	US-09-643-597-332
12	2185	91.7	2270	4	US-09-542-615A-332
					Sequence 332, App

13	2185	91.7	2270	4	US-09-630-940B-332	Sequence 332, App
14	2185	91.7	4849	3	US-09-643-597-335	Sequence 335, App
15	2185	91.7	4849	4	US-09-542-615A-335	Sequence 335, App
16	2185	91.7	4849	4	US-09-606-421B-335	Sequence 335, App
17	2185	91.7	4849	4	US-09-630-940B-335	Sequence 335, App
18	1813	76.1	1386	3	US-09-643-597-336	Sequence 336, App
19	1813	76.1	1386	4	US-09-542-615A-336	Sequence 336, App
20	1813	76.1	1386	4	US-09-606-421B-336	Sequence 336, App
21	1813	76.1	1386	4	US-09-630-940B-336	Sequence 336, App
22	1801.5	75.6	2082	3	US-09-643-597-334	Sequence 334, App
23	1801.5	75.6	2082	4	US-09-277-196-1	Sequence 1, Appli
24	1801.5	75.6	2082	4	US-09-542-615A-334	Sequence 334, App
25	1801.5	75.6	2082	4	US-09-606-421B-334	Sequence 334, App
26	1801.5	75.6	2082	4	US-09-630-940B-334	Sequence 334, App
27	1801.5	75.6	2820	3	US-09-643-597-331	Sequence 331, App
28	1801.5	75.6	2820	4	US-09-542-615A-331	Sequence 331, App
29	1801.5	75.6	2820	4	US-09-606-421B-331	Sequence 331, App
30	1801.5	75.6	2820	4	US-09-630-940B-331	Sequence 331, App
31	1793.5	75.3	4655	3	US-09-643-597-151	Sequence 151, App
32	1793.5	75.3	4655	4	US-09-480-884A-151	Sequence 151, App
33	1793.5	75.3	4655	4	US-09-542-615A-151	Sequence 151, App
34	1793.5	75.3	4655	4	US-09-606-421B-151	Sequence 151, App
35	1793.5	75.3	4655	4	US-09-221-107-151	Sequence 151, App
36	1793.5	75.3	4655	4	US-09-466-396A-151	Sequence 151, App
37	1793.5	75.3	4655	4	US-09-476-496A-151	Sequence 151, App
38	1793.5	75.3	4655	4	US-09-630-940B-151	Sequence 151, App
39	1793.5	75.3	4655	4	US-09-285-479-151	Sequence 151, App
40	765.5	32.1	1555	2	US-08-696-376-1	Sequence 1, Appli
41	753.5	31.6	1146	3	US-09-257-580-1	Sequence 4, Appli
42	753.5	31.6	1146	3	US-09-257-580-4	Sequence 4, Appli
43	724	30.4	1483	3	US-08-796-101-44	Sequence 168, App
44	724	30.4	1511	3	US-08-796-101-168	Sequence 13, Appl
45	722.5	30.3	1303	1	US-08-047-041A-13	

ALIGNMENTS

RESULT 1

US-09-949-016-5447
; Sequence 5447, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5447
; LENGTH: 2810
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5447

Alignment Scores:
Pred. No.: 1.13e-250 Length: 2810
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-670-568C-1 (1-448) x US-09-949-016-5447 (1-2810)

Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20

Db	146	ATGTCC	CAGAGC	CACAGAC	AAATGAA	TTCTC	AGTCC	AGAGG	TTTTT	CCAGCAT	ATATCG	205
Qy	21	AspPhe	LeuGlu	GlnPro	IleCys	SerVal	GlnPro	IleAsp	LeuAsn	PheVal	AspGlu	40
Db	206	GATTTT	CTGGAC	AGCCTA	TATATG	TTTCAG	TTCAGG	CCCATG	NACTT	GAACTT	TGGATGAA	265
Qy	41	ProSer	GluAsp	GlyAla	ThrAsn	LeuIle	GluLeu	SerMet	AspCys	IleArg	MetGln	60
Db	266	CCATC	AGAAGAT	GTGCG	ACAAA	CAAGATT	GAGATT	AGCAT	TGGACT	GTAT	CCGATCGAC	325
Qy	61	AspSer	AspLeu	SerAsp	ProMet	TrpPro	GlnTyr	ThrAsn	LeuGly	LeuLeu	AsnSer	80
Db	326	GACTCG	CACTG	AGTAC	CCCATG	TGGCC	CACAGTAC	ACGAAC	CTTGGG	GGCTCT	GAAACAGC	385
Qy	81	MetAsp	GlnGln	IleGln	AsnGly	SerSer	SerThr	SerPro	TyrAsn	ThrAsp	HisAla	100
Db	386	ATGACC	CAGCAG	ATTTC	AGNAC	GGGTCT	CTCGTCC	ACCACT	CCCTAT	ATAAC	CAGAC	445
Qy	101	GlnAsn	SerVal	ThrAla	ProSer	ProTyr	AlaGln	ProSer	SerThr	PheAsp	AlaLeu	120
Db	446	CAGAAC	CAGCGT	CACGG	CCCTC	CCCTC	CTAC	GCAC	CAGCC	AGCTC	CACTTCGAT	505
Qy	121	SerPro	SerPro	AlaIle	ProSer	AsnThr	AspTyr	ProGly	ProHis	SerPhe	AspVal	140
Db	506	TCTCC	ATCAC	CCCGC	ATCC	CTCC	CAAC	ACCGACT	ACC	CAGCG	CCGAC	565
Qy	141	SerPhe	GlnGln	SerSer	ThrAla	LeuSer	AlaThr	TrpThr	TyrSer	ThrGlu	LeuLys	160
Db	566	TCCTTC	CAGCAG	TCCG	ACAC	CGCC	AGCTGG	CCAC	CTTGG	AGTATT	CCACTGA	625
Qy	161	LysLeu	TyrCys	GlnIle	AlaLys	ThrCys	ProIle	GlnIle	LysVal	MetThr	ProPro	180
Db	626	AAACT	CTACT	GC	CAAT	TTG	CAAA	GACAT	GC	CCCAT	CCAGAT	685
Qy	181	ProGln	GlyAla	ValIle	IleArg	AlaMet	ProVal	Tyrls	LysAla	GluHis	ValThr	200
Db	686	CCTCAG	GGAGCT	GTATT	CCGCG	CCATC	CTGTCT	TACAAA	AAAGCT	GACG	ACGTAC	745
Qy	201	ValVal	LysArg	CysPro	AsnHis	GluLeu	SerArg	GluPhe	AsnGlu	GlyGln	IleAla	220
Db	746	GTGGT	GAAGCG	TGCCCC	CAAC	CTAG	CTGAC	TGAC	CGCTG	NAAT	TCAAC	805
Qy	221	ProPro	SerHis	LeuIle	ValArg	ValGlu	GlyAsn	SerHis	AlaGln	TyrVal	GluAsp	240
Db	806	CCTCCT	AGTCA	TTTGA	TTTCG	AGTAG	GGGAA	CAGCC	ATG	CCCAT	TATG	865
Qy	241	IleThr	GlyArg	GlnSer	ValLeu	ValPro	TyrGlu	ProPro	GlnVal	GlyThr	GluPhe	260
Db	866	ATCAC	AGAA	GACAG	AGTGT	CTCGT	TACCTT	TATG	AGCC	ACCC	AGTTG	925
Qy	261	ThrThr	ValLeu	TyrAsn	PheMet	CysAsn	SerSer	CysVal	GlyGly	MetAsn	AtqArg	280
Db	926	ACGAC	AGCTT	TGTAC	AAATTT	CA	TGTGT	AA	CAGC	AGTTGT	TGTGG	985
Qy	281	ProIle	LeuIle	IleVal	ThrLeu	GluThr	ArgAsp	GlyGln	ValLeu	GlyArg	ArgCys	300
Db	986	CCAAT	TTTAA	TCA	TTTACT	CTCG	AAAC	CAGAG	ATGG	CAAGT	CTCTG	1045
Qy	301	PheGlu	AlaArg	IleCys	AlaCys	ProGly	ArgAsp	ArgLys	AlaAsp	GluAsp	SerIle	320
Db	1046	TTTGAG	CCCGG	ATCT	GTGCT	TG	CCCA	GGAA	GAC	AGG	CGGAT	1105
Qy	321	ArgLys	GlnGln	ValSer	AspSer	ThrLys	AsnGly	AspGly	ThrLys	ArgPro	PheArg	340
Db	1106	AGAA	AGCAG	CAAGT	TTTC	CGG	CAGT	TAC	AAAG	AACCG	TATG	1165
Qy	341	GlnAsn	ThrHis	GlyIle	GlnMet	ThrSer	IleLys	LysArg	ArgSer	ProAsp	AspGlu	360
Db	1166	CAGN	ACAC	ACAT	TG	TATCC	GATCC	ATC	AGAA	ACG	AAGAT	1225
Qy	361	LeuLeu	TyrLeu	ProVal	ArgGly	ArgGlu	ThrTyr	GluMet	LeuLeu	LysIle	LysGlu	380

QY 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
DB ATGGACACAGATTCAGAAAGGCTCTCGTCCACAGTCCCTATAACACAGACGCGG 444
QY 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
DB CAGAACAGCGGTACGCGCGCTCGCTACGACAGCCAGCTCCACCTTCGATGCTCTC 504
QY 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
DB TCTCCATACCCGCGCATCCCTCCAAACCGACTACCCAGGCGCGCACAGTTTCGACG 564
QY 141 SerPheGlnGlnSerThrAlaLysSerAlaThrTyrThrSerThrGluLeuLys 160
DB TCTTCCAGCAGTCAGACACCGCAAGTCGGCCACTGGACGCTATTCCTCACTGAAG 624
QY 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
DB AAACCTCTACTGCCAAATTCGCAAGACATGCCCATCCAGATCAAGGTGATGACCCAC 684
QY 181 ProGlnGlyValAlaValIleAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
DB CCTCAGGAGCTGTTATCCGCGCATGCTGCTACAAAAAGCTGAGCACCTCAGGAG 744
QY 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
DB GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCTGAGCTGAAATTCACGAGGACAGATTGCC 804
QY 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
DB CCTCTAGTCACTTGTATTCAGTAGAGGGAACAGCCAGTATGTAGAGGATGAACCGCGT 864
QY 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
DB ATCAGAGGAAGACAGAGTGTGTGTACCTTATGAGCCACCCAGCTGGCACTGAATTC 924
QY 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyMetAsnArgArg 280
DB AGACAGCTCTTGTACAAATTCATGTGTACAGCAGTTGTGTGGAGGATGAACCGCGT 984
QY 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
DB CCAATTTTAACTGTTACTCTGGAACACAGAGATGGCAAGTCTCGGCGCGAGCTGC 1044
QY 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
DB TTTGAGGCGCGATCTGTCTGTCGCCAGGAAGAGACAGGAAGCGGATGAAGATGATC 1104
QY 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
DB AGAAGCAGCAAGTTTCGACAGTACAAAGACGGTGTGTGACGAGCGCGCTTCTGT 1164
QY 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgSerProAspAspGlu 360
DB CAGAACACACATGTTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGAA 1224
QY 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysLysGlu 380
DB CTGTTATACTTACCACTGAGGCGCGTGAGACTTATGAAATGCTGTGTAAGATCAAGAG 1284
QY 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
DB TCCCTGGAACTCATGACGATACCTTCTCTCAGCACACAAATTTGAAACGTACAGGCAAG 1344
QY 401 GlnGlnGlnHisGlnLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
DB CAGCAGCAGCAGCAGCAGTCTTCTCAGAAACATCTCTTTCAGCTGCTTTCAGGAATGAG 1404
QY 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
DB CTTGTGAGCGCGGAGAGAACTCCAAACAACTCTGAGCTCTTCTTTAGACATTCAGAG 1464
QY 441 ProProAsnArgSerValTyrPro 448

DB 1465 CCCCCAAACCGATCAGTGTACCCA 1488
RESULT 3
US-09-542-615A-333
; Sequence 333, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Pan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-333
Alignment Scores:
Pred. No.: 1,136-250 Length: 2816
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-670-568c-1 (1-448) x US-09-542-615A-333 (1-2816)
QY 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTyr 20
DB 145 ATGTCCTCCAGACACACAGCAATGAATTCCTCAGTCACGAGGTTTTCAGCATATCTGG 204
QY 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
DB 205 GATTTTCTGGAAACAGCTATATGTTTCAGTTCAGCCCATTTGACTTGAATTCGATGAA 264
QY 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
DB 265 CCATCAGAAAGATGGTGGCACAACAAAGATTGAGATTAGCATGTGATCCGATGCGAG 324
QY 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
DB 325 GACTCGGACCTGAGTGACCCCGATGTGGCCACAGTACAGAACCTTGGGGCTCCTGAACAGC 384
QY 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
DB 385 ATGGACACAGCATTCAGAAAGGCTCTCGTCCAGCAGTCCCTATAACACAGACGCGG 444
QY 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
DB 445 CAGAACAGCGTACGCGCGCTCGGCCCTACGACAGCCAGCTCCACCTTCGATGCTCTC 504
QY 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
DB 505 TCTCCATACCCGCGCATCCCTCCAAACCGACTACCCAGGCGCGCACAGTTTCGACG 564
QY 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrSerThrGluLeuLys 160
DB 565 TCTTCCAGCAGTCAGACACCGCAAGTCGGCCACTGGACGCTATTCCTCACTGAAG 624
QY 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
DB 625 AAACCTCTACTGCCAAATTCGCAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT 684

```
QY 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTTATTCGGCCCATCTGCTCTACAAAAGCTGAGCACGTCACGGAG 744
QY 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCACAGGAGCAGATTGCC 804
QY 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CCTCCTAGTCAATTTGATTTCAGTAGAGGGGAACAGCCATGCCAGTATGTAGAAGATCCC 864
QY 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCACAGGAGACAGAGTGTGCTGTACCTTATGAGCCACCCAGGTTGGCACTGATTC 924
QY 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 AGCACAGTCTTGTAACATTTTCATGTAAACAGCAGTGTGTGGAGGGATGAACCGCCGT 984
QY 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgCys 300
Db 985 CCAATTTTAAATCATTTGTTACTTGGAAACAGAGATGGGCAAGTCTGGGCCGAGCCTGC 1044
QY 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGCCCGGATCTGTCTTGGCCAGGAGACAGGAGCGGATGAAGATAGCATC 1104
QY 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGGACAGTCAAAAGAACCGTGATGGTACGAAGCGCCGTTTCGT 1164
QY 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGTTGATCCAGATGATCCATCAAGAAACGAAGATCCCGCATGATGAA 1224
QY 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLysIleLysGlu 380
Db 1225 CTGTTATATTACCTAGAGGGCCGTGAGACTTATGAATGCTGTTGAAGATCAAGAG 1284
QY 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1285 TCCCTTGGAACTCATGCACTACCTTCTCAGCACACAAATTTGAAACGTACAGGCAACAGCAA 1344
QY 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCAGCAGCAGTCTTACTTCAGAAACATCTCTTTTCAGCCCTGCTTCAGGAATGAG 1404
QY 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1405 CTGTGTGAGCCCGGAGAGAACTCCAAACAACTCTGACGCTCTCTTTAGACATTTCCAAG 1464
QY 441 ProProAsnArgSerValTyrPro 448
Db 1465 CCCCCAAACCGATCAGTGATCCCA 1488
```

RESULT 4

```
US-09-606-421B-333
; Sequence 333, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
```

```
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-606-421B-333

Alignment Scores:
Pred. No.: 1,13e-250 Length: 2816
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-670-568C-1 (1-448) x US-09-606-421B-333 (1-2816)
QY 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTyr 20
Db 145 ATGTCCTCCAGAGCAGACACAGCAATGAATCTTCAGTCCAGAGTTTTCAGCATATCTGG 204
QY 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGAAACAGCCTATATGTTTCAGTTCAGCCCATTTGACTTGAACCTTTGTGATGAA 264
QY 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 265 CCATCAGAAAGATGGTGGCAGCAAAACAAAGATTGAGATTAGCATGGACTGTATCCGCATGCGAG 324
QY 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACCTGGGGCTCTCTGACACAGC 384
QY 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGGACACAGCAGATTTCAGAACGGCTCTCTCGTCCACAGTCCCTATTAACACAGACACACGCG 444
QY 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACACGCGTCACGGCCCTTCGCCCTACGCACAGCCAGCTCCACCTTCGATGCTCTC 504
QY 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCCGCCCATCTCCCTCCAACACCGACTACCCAGGCCGCGCACAGTTTCGACGTC 564
QY 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
Db 565 TCCTTCCAGCAGTCGAGCACCGCCCAAGTCCGCCACCTGGACGCTATTTCCACTGAACCTGAAG 624
QY 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACCTTACTGCCAAATTCGAAAGACATGCCCATTCAGATCAAGGTGATGATACCCCACT 684
QY 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTTATTCGGCCCATGCTGCTACAAAAGAGTTCAGCACGTCACGGAG 744
QY 201 ValValLysArgCysProAsnHisGlnLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCACAGGAGGAGCAGATTGCC 804
QY 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CCTCCTAGTCAATTTGATTTCAGTAGAGGGGAACAGCCATGCCAGTATGTAGAAGATCCC 864
QY 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCACAGGAGACAGAGTGTGCTGTATGAGCCACCCAGGTTGGCACTGATTC 924
QY 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
```

```
Db 925 ACGACAGCTCTGTGTAACAATTCATGTGTAAACAGCAGCTGTGTGGAGGATGAACCGCGT 984
Qy 281 ProIleLeuIleValThrLeuThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 985 CCAATTTTAAATCATTTACTCTGGAACCAAGAGATGGCAAGTCTTGGCCGACGCTGC 1044
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerile 320
Db 1045 TTTGAGGCCGGATCTGTCTTCCAGGAAGAGACAGAGAGCGGATGAAGATAGCATC 1104
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgPropheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAAACGGTGATGTGACGAAGCCCGTTTCGT 1164
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA 1224
Qy 361 LeuLeuValLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1225 CTGTTTACTTACAGTGGAGGGCGGTGAGCTTATGAAATGCTGTGGAAGATCAAGAG 1284
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGln 400
Db 1285 TCCCTGGAACCTCATGCAGTACCTCTCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCACACAGCACTTACTTTCAGAAACATCTCTTTTCAGGCTGTGTTTCAGGAATGAG 1404
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1405 CTGTGGAGCCCCGGAGAGAAATCCAAACAACTGACGCTCTCTTTAGACATTCCTCAAG 1464
Qy 441 ProProAsnArgSerValTyrPro 448
Db 1465 CCCCCAAACCGATCAGTGTATCCCA 1488

RESULT 5
; Sequence 333, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630.940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-333

Alignment Scores:
Pred. No.: 1,13e-250 Length: 2816
Score: 2383.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
```

```
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-670-568C-1 (1-448) x US-09-630-940B-333 (1-2816)
Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db 145 ATGTCCAGAGCAGACAGCAATGAATTCCTCAGTCAGAGGTTTCCAGCATATCTCG 204
Qy 21 AspPheLeuGlnProlIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTCTGAACACGCTATATGTTTCAGTTTCAGCCCATGACTTGAATCTTGTGGATGA 264
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluLysSerMetAspCysIleArgMetGln 60
Db 265 CCATCAGAAAGATGGTGGCAGACAAACAGATTGAGATTAGCATGGACTGTATCCGATGCG 324
Qy 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCCTGAACAGC 384
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGGACAGCAGATTCAGAACGGCTCCTCGTCCACCATGCTTATAACACAGACACGCG 444
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACAGCTCAGGGCGCTCGCCCTACGACAGCCAGCTCCACTTCGATGCTCTC 504
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCCGCTATCCCTCCACACAGCTACCCAGCCCGCACAGTTTCGACGCTG 564
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db 565 TCCTTCAGCAGTCGAGCAGCGCCAGTCCGCGCACCTGGACAGTATCCACTGAACTGAAG 624
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAATCTACTGCCAATTTGCAAGACATGCCCATCCAGATCAGGTGTAGTACCCCACT 684
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGGAGCTGTATTCGCGGCATCGCTGTCTACAAAAAGCTGAGCAGCTCAGCGAG 744
Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTTCAACGAGGGGACAGATTGCC 804
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CTCTCTAGTATTTGATTTCAGTAGAGGGGAACGCCATGCCCATGATGTAGAAAGATCCC 864
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 865 ATCAGAGGAAGACAGAGTGTGCTGTTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 924
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACGACAGCTCTGTACAAATTTTCATGTGTAAACAGCAGTTGTGTGGAGGGATGAACCGCGT 984
Qy 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 985 CCAATTTTAAATCATTTACTCTGGAACCAAGAGATGGCAAGTCTTGGCCGACGCTGC 1044
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerile 320
Db 1045 TTTGAGGCCGGATCTGTGCTTCCAGGAAGAGACAGAGAGCGGATGAAGATAGCATC 1104
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgPropheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAAACGGTGATGTGACGAAGCCCGTTTCGT 1164
```

QY 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLeuArgSerProAspGlu 360
|||
Db 1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAAGAGATCCCCAGATGAA 1224
|||
QY 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysLeuGlu 380
|||
Db 1225 CTGTTATACCTTACCAGTGAGGGCCCGTGAGACTTATGAATGCTGTGAAGATCAAAGAG 1284
|||
QY 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGln 400
|||
Db 1285 TCCTTGGAACTCATGACGATACCTTCTCTCAGCACACAATGAAACGTACAGGCAACAGCAA 1344
|||
QY 401 GlnGlnGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
|||
Db 1345 CAGCAGCAGCAGCAGCAGCTTACTTCAGAAACATCTCTTTCAGCCTGCTTCAGGAATGAG 1404
|||
QY 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
|||
Db 1405 CTGTGGAGCCCGGAGAGAACTCCAAACAACTCTGACGTCTTCTTAGACATTCACAG 1464
|||
QY 441 ProProAsnArgSerValTyrPro 448
|||
Db 1465 CCCCCAAACCCATCAGTGATCCCA 1488
|||

RESULT 6

US-09-643-597-337
; Sequence 337, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 337
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-337

Alignment Scores:
Pred. No.: 2,21e-229 Length: 1551
Score: 2185.00 Matches: 416
Percent Similarity: 94.80% Conservative: 3
Best Local Similarity: 94.12% Mismatches: 7
Query Match: 91.69% Indels: 16
DB: 3 Gaps: 1

US-09-670-568C-1 (1-448) x US-09-643-597-337 (1-1551)

QY 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
|||
Db 1 ATGTCCAGAGACACAGACAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG 60
|||
QY 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
|||
Db 61 GATTTCTGGAAACAGCCTATATGTTGAGTTTCAGCCCATTTGACCTTGAACCTTTGGATGAA 120
|||
QY 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
|||

Db 121 CCATCAGAAGATGGTGGCAGCAAAACAAGATTGAGATTAGACTGATCGCATGCAG 180
|||
QY 61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
|||
Db 181 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACCTGGGGCTCTCGAACAGC 240
|||
QY 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
|||
Db 241 ATGGACACAGCAGATTCAAGACGGCTCTCGTCCACAGTCCCTATAACACACACACCGCG 300
|||
QY 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
|||
Db 301 CAGAACACGCGTCACGGCCCTCGCCCTACGACACAGCCAGCTCCACCTTCGATGCTCTC 360
|||
QY 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
|||
Db 361 TCTCATCATCCCGCCCATCCCTTCCAAACCCAGTACCCAGGCCCGCACAGTTTCACGCTG 420
|||
QY 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
|||
Db 421 TCCTTCCAGCAGCTCGAGCACCGCCCAAGTCGGCCACCTGGACGTATTCCACTGAACCTGAAG 480
|||
QY 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
|||
Db 481 AAACCTCTACTGCCAAATTCNAAGACATGCCCCATCCAGATCAAGGTGATGACCCACCT 540
|||
QY 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
|||
Db 541 CCTCAGGGAGCTGTATCCGGGCCATGCTGTCTACAAAAAAGCTGAGCACCTCAGCGAG 600
|||
QY 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
|||
Db 601 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCGCTGAATTCACAGAGGAGCAGATTGGC 660
|||
QY 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
|||
Db 661 CCTCTAGTCACTTTGATTTCGAGTAGAGGGGAACGCCATGCCAGTATGTGAAGATCCC 720
|||
QY 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
|||
Db 721 ATCAGGAAGACAGAGTGCTGTGTACTTATGAGCCACCCAGGTTGGCACTGAATTC 780
|||
QY 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
|||
Db 781 ACGACAGCTCTGTACAAATTCATGTGTAAACAGCAGTGTGTGTGGAGGAGTAAACCGCGT 840
|||
QY 281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
|||
Db 841 CCAATTTTAAATCATTTGTTACTCTGGAAACCCAGAGATGGGCAAGTCTCTGGCCGACGCTGC 900
|||
QY 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
|||
Db 901 TTTGAGGCCCGGATCTGTGCTTGGCCAGGAAGACAGACAGGCGGATGAAGATAGCATC 960
|||
QY 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
|||
Db 961 AGAAAGCAGCAAGTTTCGACAGTACAAAGAACGGTGATGGTACGAGCGCCGCTTTCGT 1020
|||
QY 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
|||
Db 1021 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCATGATGAA 1080
|||
QY 361 LeuLeuTyrLeuProValArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
|||
Db 1081 CTGTTATCTTACCAGTGAGGGCGGTGAGACTTATGAATGCTGTTGAAGATCAAAGAG 1140
|||
QY 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGln 400
|||
Db 1141 TCCCTGGAACTCATGCAGTACCTCTCCTCAGCACAAATTTGAAACGTTACAGGCAACAGCAA 1200
|||
QY 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
|||
Db 1201 CAGCAGCAGCAGCAGCAGCTTACTTTCAGAAA----- 1230
|||


```
Qy 421 LeuValGluProArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1231 -----CAGACCTCAATACAGTCTCCATCTTATATGTTAAAGCTCC 1272
Qy 441 ProPro 442
Db 1273 CCACCT 1278

RESULT 7
US-09-542-615A-337
; Sequence 337, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 337
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-337

Alignment Scores:
Pred. No.: 2,21e-229 Length: 1551
Score: 2185.00 Matches: 416
Percent Similarity: 94.80% Conservative: 3
Best Local Similarity: 94.12% Mismatches: 7
Query Match: 91.69% Indels: 16
DB: Gaps: 1

US-09-670-568C-1 (1-448) x US-09-542-615A-337 (1-1551)
Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTyr 20
Db 1 ATGTCCAGAGCACACAGACAAATGATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG 60
Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 61 GATTTTCTGGAACAGCCTATATGTTTCAAGTTCAGGCCCATTTGACTTGAACCTTTGTGGATGAA 120
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 121 CCATCAGAAGATGTTGGCACAACAAAGATTGAGATTAGCATGGAGCTGTATCCCGATCGAG 180
Qy 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 181 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACCTTGGGGCTCTCTGAACAGC 240
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 241 ATGGACACAGCATTCAGAACGGCTCTCTGTCACACAGTCCCTATACACAGACACACGCG 300
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 301 CAGAACAGCGTCACGGGGCCCTCGCCCTTACGACAGGCCAGCTCCACCTTCGATGCTCTC 360
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 361 TCTCATCACCCCGCATCCCTCCACACCCGACTTACCAGGCCCGCAGAGTTTCGAGCTG 420
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
Db 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
```

```
Db 421 TCCTTCAGCAGTCGAGCACCGCCAGTCCGACCTGGACCTATTCACCTGAACTGAAG 480
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 481 AAATCTTACTTGCACAAATTTGCAAGACATGCCCATCCAGATCAAGGTGATGACCCCACT 540
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 541 CCTCAGGGAGCTGTATTCGCGGCATGCTCTACAAAAAAGCTGAGCAGCTCACGAG 600
Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 601 GTGGTGAAGCGGTGCCCCAAGCATGAGCTGAGCGCTGAATTTCAACGAGGGACAGATTGCC 660
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 661 CCTCCTAGTTCATTTGATTTCGAGTAGAGGGGAACAGCCATGCCCATGTATGAGAAGATCCC 720
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 721 ATCAGAGGAAGACAGAGTGTGCTGTTACCTTATGAGCCACCCACAGTTGGCACTGAATTC 780
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 781 ACGACAGCTCTTGTACAAATTTTATGTTTAAACAGCAGTTGTGTGGAGGGATGAACCGCGT 840
Qy 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 841 CCAATTTTAAATCATTTGTTACTCTGGAAACAGAGATGGCAAGTCTCTGGCGCCGACGTGC 900
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 901 TTTGAGGCCCGGATCTGTGCTTCCCCAGGAAGACAGAGAGGCGGATGAAGATAGCATC 960
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgPropheArg 340
Db 961 AGAAAGCAGCAAGTTTTCGAGCAGTACAAAGAACGGTGTATGTAATGCTGTTGAAGATCAAAGAG 1020
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1021 CAGAACACATCGTATCCAGATGACATCCATCAAGAAACGAGATCCCCAGATGATGAA 1080
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1081 CTGTTATATTACAGTGAGGCGCGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1140
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1141 TCCCTGGAACTCATGAGTACCTTCTCAGCACACAATTTGAAACGTACAGGCAACAGCAA 1200
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1201 CAGCAGCAGCAGCAGCAGCTTACTTTCAGAAA----- 1230
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1231 -----CAGACCTCAATACAGTCTCCATCTTTCATATGTTAAAGCTCC 1272
Qy 441 ProPro 442
Db 1273 CCACCT 1278

RESULT 8
US-09-606-421B-337
; Sequence 337, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
```

APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 337
LENGTH: 1551
TYPE: DNA
ORGANISM: Homo sapiens
US-09-606-421B-337

Alignment Scores:
Pred. No.: 2,21e-229 Length: 1551
Score: 2185.00 Matches: 416
Percent Similarity: 94.80% Conservative: 3
Best Local Similarity: 94.12% Mismatches: 7
Query Match: 91.69% Indels: 16
DB: 4 Gaps: 1

US-09-670-568C-1 (1-448) x US-09-606-421B-337 (1-1551)

```
Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db 1 ATGTCCAGAGCACACAGACAAATGAAATTCCTCAGTCAGAGGTTTTCACGACATATCTGG 60
Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 61 GATTTCTGGAAACGCTATATGTTAGTTCAGGCCCATGACTGAACTTGTGGATGAA 120
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluLeuSerMetAspCysIleArgMetGln 60
Db 121 CCATCAGAAGATGTGGCACAACAAGATTGAGATTAGCATGAGTGTATCCCGCATCGAG 180
Qy 61 AspSerAspLeuSerAspProMetTrpProGlnThrThrAsnLeuGlyLeuAsnSer 80
Db 181 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACCTGGGGCTCCTGAACAGC 240
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 241 ATGACACAGACAGATTGACAGCGCTCTCTGTCACACAGCTCCCTATACACAGACACGCG 300
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 301 CAGAACAGCGTCAGGGGCGCCCTCGCCCTACGCACAGCCAGCTCCACCTTCGATGCTCTC 360
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 361 TCTCCATCACCCGGCATCCCTCTCAACACCCAGTACCCAGGCCCGCCAGAGTTTCGAGCGT 420
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrThrSerThrGluLeuLys 160
Db 421 TCCTTCACGAGCTGAGACACCGCCAGTCCGCCACCTGGAGGTATTCACCTGAACCTGAG 480
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 481 AAACCTTACTGCCAAATTTGCAAGACATGCCCTCCATCCAGATCAAGGTGATGACCCCACT 540
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 541 CCTCAGGGAGCTGTATTCGGGGCCATGCTCTCTACAAAAAAGCTGAGCAGCTCAGCGAG 600
Qy 201 ValValLysArgCysProAsnHisGlnLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 601 GTGTGTAAGCCGTCGCCCAACCATGAGCTGAGCCGTGAATTCACAGGGGACAGATTGCC 660
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 661 CCTCCTAGTCAATTTGATTCGAGTAGAGGGGAACAGCCATGCCAGTATGTAGAGATCCC 720
```

```
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
Db 721 ATCAGAGGAAGACAGAGTGTGCTGGTACCTTATGAGCCACCCAGGTTGGCAGTGAATTC 780
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 781 ACGACAGCTCTGTGTACAAATTTTCATGTGTAAACAGCAGTGTGTGTGGAGGATGAACCGCGT 840
Qy 281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 841 CCAATTTTATCATTTGTTACTCTGGAAACCCAGAGATGGGCAAGTCTCTGGGCCGAGCGTGC 900
Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 901 TTTGAGGCCCGGATCTGTCTGCCAGGAAGACAGACAGGAAGCGGATGAAGATAGCATC 960
Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 961 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGTGTGTTAGAAATGCTGTTGAAGATCAAGAG 1020
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1021 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAAGATCCCCAGATGATGAA 1080
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1081 CTGTTATATTACAGTACAGTGGGCGCTGAGACTTATGAATGCTGTTGAAGATCAAGAG 1140
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1141 TCCTCGAAGCTCATGTCAGTACCTTCCTCAGCACACAAATTTGAAACGTACAGGCAACAGCAA 1200
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1201 CAGCAGAGCAGCAGCAGCTTACTTTCAGAAA-----CAGACCTCAATACAGTCTCCATCTTCAATATGTTAAACAGTCC 1272
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1231 -----CAGACCTCAATACAGTCTCCATCTTCAATATGTTAAACAGTCC 1272
Qy 441 ProPro 442
Db 1273 CCACCT 1278
RESULT 9
US-09-630-940B-337
; Sequence 337, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 337
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-337
```

Alignment Scores:
Pred. No.: 2,21e-229 Length: 1551
Score: 2185.00 Matches: 416
Percent Similarity: 94.80% Conservative: 3
Best Local Similarity: 94.12% Mismatches: 7
Query Match: 91.69% Indels: 16
DB: 4 Gaps: 1

US-09-670-568C-1 (1-448) x US-09-630-940B-337 (1-1551)

Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db 1 ATGTCCCAAGACACACAGACAAATGAATTCCTCAGTCAGAGAGTTTCCAGCATATCTGG 60

Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 61 GATTTTCTGGAAACACCCCTATATGTTTCAGTTGAGCCCATGACTTGAATCTTTGTGGATGAA 120

Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 121 CCATCAGAAGATGTTGCGACAAACAGATTGAGATTAGCATGGACTGTATCCGCGATGCG 180

Qy 61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 181 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACACGAACCTTGGGGCTCTCTGAACAGC 240

Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 241 ATGACACAGCAGATTTCAGAACGGCTCTCTGCTCCACCATGCTCTATAACACAGACCGCG 300

Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 301 CAGAACAGCGTCACGGCGCCCTCGCCCTACGCACAGCCCGCTCCACCTTCGATGCTCTC 360

Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 361 TCTCCATCACC CGCATCCCTCCAAACACCGACTACCCAGCGCCGCGACAGTTTCGACGTG 420

Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
Db 421 TCCTTCCAGCAGTCGAGCACC CGCAAGTCGGCCACCTCGGACGTATTCACATGAACCTGA 480

Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 481 AAATCTACTGCCAAATGCAAGACATGCCCATCCAGATCAAGTGATGATGCCCCACCT 540

Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 541 CCTCAGGAGCTGTATTCGGCGCCATGCTCTACAAAAAAGCTGAGCACGTCAACGCG 600

Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 601 GTGTGAAGCGGTGCCCCCAACCATGAGCTGAGCGGTGAATTCACAGGGGACAGATTGCC 660

Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 661 CCTCTAGTCAATTTGATTCGAGTAGGGGGAACGCCCATGCCAGTATGTAGAGATCCC 720

Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
Db 721 ATCAGAGGAACAGAGAGTGTCTGGTACCTTATGAGCCACCCAGGTGGCACTGAATTC 780

Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 781 ACGACAGCTTTGTGTAATTTTCATGTGTAAACAGCAGTTGTGTGGAGGGATGAACCGCGT 840

Qy 281 ProfileLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 841 CCAATTTTAATCATTTGTTTACTTCTGAAACACAGAGATGGCGAAGTCTTGGGCCGACGTGC 900

Qy 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 145 ATGTCCAGAGCACACAGACAAATGAATTCCTCAGTCAGGAGTTTCCAGCATATCTGG 204

Db 901 TTTGAGGCCCGGATCTGTGCTTGCCAGGAAGAGACAGAAAGCGGATGAAGATAGCATC 960

Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 961 AGAAGCAGCAAGTTTCGACAGGTACAAAGAACCGGTGTGTAGAACGCCCGCTTCGT 1020

Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1021 CAGAACACACATGTTATCCAGATGACATCCATCAAGAAACCAAGATCCCCAGATGATGAA 1080

Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1081 CTGTTATATCTTACCAGTGAGGGCGCTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1140

Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Db 1141 TCCCTGGAACCTCATGCACTACCTTCTCCAGCACAAATTTGAACGTACAGGCAACAGCAA 1200

Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1201 CAGCAGCAGCAGCAGCAGCAGCTTACTTCAGAAA----- 1230

Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1231 -----CAGACCTCAATACAGTCTCCATCTTCATATGTTAAACAGCTCC 1272

Qy 441 ProPro 442
Db 1273 CCACCT 1278

RESULT 10
US-09-643-597-332
; Sequence 332, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-332

Alignment Scores:
Pred. No.: 4,16e-229 Length: 2270
Score: 2185.00 Matches: 416
Percent Similarity: 94.80% Conservative: 3
Best Local Similarity: 94.12% Mismatches: 7
Query Match: 91.69% Indels: 16
DB: 3 Gaps: 1

US-09-670-568C-1 (1-448) x US-09-643-597-332 (1-2270)

Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db 145 ATGTCCAGAGCACACAGACAAATGAATTCCTCAGTCAGGAGTTTCCAGCATATCTGG 204

```
QY 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
DB 205 GATTTTCTGGAACAGCTATATGTTTCAGTTTTCAGCCATTGACTTGAATTTTGTGGATGAA 264
QY 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
DB 265 CCATCAGAAAGATGTTGCGCAAAACAAGATTGAGATTAGCATGGACTGTATATCCGCGATGCG 324
QY 61 AspSerAspLeuSerAspProMetTTPProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
DB 325 GACTCGGACCTGAGTGACCCCATGTTGGCCACAGTACACGAACTGGGGCTCTTGACACGC 384
QY 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
DB 385 ATGGACACAGATTGAGAAACGGCTCTCGTCCACCACTCCCTATATAACACAGACACGCG 444
QY 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
DB 445 CAGAACAGCGTACGGCGCCCTCGCCCTACGCACAGACAGCCAGCTCCACCTTCGATGCTCTC 504
QY 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
DB 505 TCTCCATACCCCGCATCCCTCCAAACCCGACTACCCAGGCCCGCACAGTTTCGACGTG 564
QY 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
DB 565 TCTTCCAGCAGTCGAGCACCGCCCAAGTCGGCCACCTGGACGTTATCCACTGAACCTGAAG 624
QY 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
DB 625 AAACCTCTACTGCCAAATTGCAAGACATGCCCATCCAGATCAAGGTGATGACCCCACT 684
QY 181 ProGlnGlnValAlaIleAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
DB 685 CCTCAGGAGCTGTATTCGGCCCATGCTGTCTACAAAAGAGCTGAGCACGTCACGGAG 744
QY 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
DB 745 GTGGTGAACGGTGGCCCAACCATGAGCTGAGCCGTGAATTCAGAGGGACAGATTGCC 804
QY 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
DB 805 CCTCTAGTCAATTTGATTCAGTAGAGGGGAAACAGCCATGCCAGTATGTAAGAATGCC 864
QY 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
DB 865 ATCACAGGAAGACAGATGTGTGTGTACCTTATGACCCACCCAGGTTGGCACTGAAATTC 924
QY 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
DB 925 ACGACAGTCTTGTAACATTTTCATGTGTAACAGCAGTGTGTGGAGGGATGAACCGCGT 984
QY 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
DB 985 CCAATTTTAAATCATTTGTTCTCGAAACACAGAGATGGGCAAGTCTCTGGCCGCGAGCTGC 1044
QY 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
DB 1045 TTGAGGCCCGGATCTGTGCTTCCCGAAGAGACAGAGGAGCGGATGAAATGATGATC 1104
QY 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
DB 1105 AGAAGACAGCAAGTTTCGGACAGTACAAAGACGGTGATGGTACGAAGCGCCGTTTCT 1164
QY 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
DB 1165 CAGAACACACATGTTATCCAGATGATCATCATCAGAAACGAAGATCCCCAGATGATGAA 1224
QY 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
DB 1225 CTGTTATATCTTACCAGTAGGGGCCGTGAGACTTTATGAATGCTGTTGAAGATCAAGAG 1284
QY 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGln 400
```

```
DB 1285 TCCCTGGAACTCATGCAGTAGCTTCTCTCAGCACAAATTGAAACGTACAGGCAACAGCAA 1344
QY 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
DB 1345 CAGCAGCAGCAGCAGCAGCAGCTTACTTCAGAAA----- 1374
QY 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
DB 1375 -----CAGACCTCAATACAGTCTCCATCTTCATATGTTAAGAACAGCTCC 1416
QY 441 ProPro 442
DB 1417 CCACCT 1422

RESULT 11
US-09-542-615A-332
; Sequence 332, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hosken, Nancy A.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-332

Alignment Scores:
Pred. No.: 4,16e-229 Length: 2270
Score: 2185.00 Matches: 416
Percent Similarity: 94.80% Conservative: 3
Best Local Similarity: 94.12% Mismatches: 7
Query Match: 91.69% Indels: 16
DB: 4 Gaps: 1

US-09-670-568C-1 (1-448) x US-09-542-615A-332 (1-2270)
QY 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
DB 145 ATGTCCAGAGACACACACACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG 204
QY 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
DB 205 GATTTTCTGGAACAGCTATATGTTTCAGTTTTCAGCCATTGACTTGAATTTTGTGGATGAA 264
QY 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
DB 265 CCATCAGAAAGATGTTGCGCAAAACAAGATTGAGATTAGCATGGACTGTATATCCGCGATGCG 324
QY 61 AspSerAspLeuSerAspProMetTTPProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
DB 325 GACTCGGACCTGAGTGACCCCATGTTGGCCACAGTACACGAACTGGGGCTCTTGACACGC 384
QY 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
DB 385 ATGGACACAGATTGAGAAACGGCTCTCGTCCACCACTCCCTATATAACACAGACACGCG 444
QY 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
DB 445 CAGAACAGCGTACGGCGCCCTCGCCCTACGCACAGACAGCCAGCTCCACCTTCGATGCTCTC 504
```

```
QY 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATACCCGCGCATCCCTCCACACCGAGTACCAGGCCGCGCACAGTTTCGACGNG 564
QY 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
Db 565 TCTCTCCAGCAGTCGAGCAGCGCCCAAGTCGGCCACCTGGACGCTATTCCACTGAACCTGAAG 624
QY 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACCTACTGCCAAATTCGAAAGACATGCCCATCCAGATCAGGTGATGACCCACCT 584
QY 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTTATCCGCGCATGCTGTCTACAAAAAGCTGAGCACGTCACGGAG 744
QY 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCAACGAGGACAGATTGCC 804
QY 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CTTCTAGTCATTTGATTCAGTAGAGGGGAACAGCCATGCCAGTATGTAGAATGCC 864
QY 241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
Db 865 ATCAGAGGAAGACAGAGTGTGTGTACCTTATGAGCCACCCAGGTTGGCACTGAATTC 924
QY 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACGACAGCTCTGTACAAATTTCTATGTGTAAACAGCAGTTGTGTGGAGGATGAACCGCGCT 984
QY 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 985 CCAATTTTAAATCATTTACTCTGGAACACAGAGATGGGCAAGTCTGGGCGAGCGCTGC 1044
QY 301 PheGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCGCGATCTGTCTTGGCCAGGACAGACAGGAGCGGATGAAGATAGCATC 1104
QY 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGGACACAGTACAAAGAACGGGTGATGGTACGAAGCGCGCTTCT 1164
QY 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAGATCCCAAGATGATGAA 1224
QY 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLysIleLysGlu 380
Db 1225 CTGTATATCTTACCAGTGAGGGCGGTGAGACTTATGAATCTGTGTTGAAGATCAAGAG 1284
QY 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGln 400
Db 1285 TCCCTGGAACTCATGCAGTACCTTCTCTCAGCACACAAATTTGAAACGCTACAGGCAACAGCAA 1344
QY 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCACAGCACTTACTTCAGAAA----- 1374
QY 421 LeuValGluProArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1375 -----CAGACCTCAATACAGTCTCCATCTTCATATGGTAAACAGCTCC 1416
QY 441 ProPro 442
Db 1417 CCACCT 1422
```

RESULT 12

US-09-606-421B-332
; Sequence 332, Application US/09606421B

; Patent No. 6531315

; GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Pan, Ligu
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 332
LENGTH: 2270
TYPE: DNA
ORGANISM: Homo sapiens
US-09-606-421B-332

Alignment Scores:
Pred. No.: 4,16e-229 ; Length: 2270
Score: 2185.00 ; Matches: 416
Percent Similarity: 94.80% ; Conservative: 3
Best Local Similarity: 94.12% ; Mismatches: 7
Query Match: 91.69% ; Indels: 16
DB: 4 ; Gaps: 1

US-09-670-568C-1 (1-448) x US-09-606-421B-332 (1-2270)

```
QY 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTyr 20
Db 145 ATGCCCCAGAGACACACAGAAATGAATTCCTCAGTCAGAGGTTTTCAGCATATCTCG 204
QY 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGAACAGCCTATATGTTTCAGTTTCAGCCCCATTGACTTGAATTTGTGGATGA 264
QY 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 265 CCATCAGAAAGATGGTGCACAAACAAAGATTGAGATTAGCATGGACTGTATCCGCATGCA 324
QY 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACTGGGGCTCTGAACAGC 384
QY 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGACACAGCAGATTTCAGAACGGCTCCTCGTCCACAGTCCCTATAACACACACACGCG 444
QY 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACACGCTCAGCGGCCCTCGCCCTACGCACAGCCAGCTCCACCTTCGATGCTCTC 504
QY 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATACCCCGCATCCCTCCAAACACGAGTACCCAGGCCCCGACAGTTTTCACGCTG 564
QY 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
Db 565 TCTTTCAGCAGCTGAGCAGCCGCAAGTCGGCCACCTTCGACGTATTTCACCTGAACCTGA 624
QY 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACCTACTGCCAAATTCGAAAGACATGCCCATCCAGATCAGGTGATGACCCACCT 684
QY 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTTATCCGCGCATGCTGTCTACAAAAAGCTGAGCACGTCACGGAG 744
QY 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
```

```
Db 745 GTGGTGAAGCGGTGCCCCAACCATGAGCTGAGCGGTGAATTCACAGGAGCAGATTGCC 804
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CTCTCTAGTCATTGTGATTGAGTAGAGGGGAACAGCCATGCCAGTATAGAAATGCC 864
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
Db 865 ATCACAGGAGACAGAGTGTGTGCTTATGAGCCACCCAGGTTGGCTGATTC 924
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACCACAGCTCTGTACAAATTCATGTGTAACAGCAGTGTGTGGAGGGATGAACCGCGT 984
Qy 281 ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgCys 300
Db 985 CCAATTTTAAATCATTTACTCTGGAACACAGAGATGGCAAGTCTGTGGCCGACGCTGC 1044
Qy 301 PheGluAlaArgIleCysAlaCysProGlyValArgAspAlaGlyAlaAspGluAspSerIle 320
Db 1045 TTTGAGCCCGGATCTGTCTTCCAGGAGAGACAGGAGCGGATGAAGATAGCATC 1104
Qy 321 ArgGlyGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAAGCAGCAAGTTTCGGACAGTACAAAGAACGGGTGATGGTACGAAGCGCGCTTCTGT 1164
Qy 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGGTATCCAGATGATCATCCATCAAGAAACGAAGATCCCCAGATGATGAA 1224
Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysIleLysGlu 380
Db 1225 CTGTTATATTACAGTGAGGGCGGTGAGACTTATGAATGCTGTGAGATCAAGAG 1284
Qy 381 SerLeuGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGln 400
Db 1285 TCCCTGGAACTCATGCAGTACCTTCTCAGCACACAAATGAAACGTACAGGCAACAGCAA 1344
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCAGCAGCAGCTACTTTCAGAAA----- 1374
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPheArgHisSerLys 440
Db 1375 -----CAGACCTCAATACAGTCTCCATCTCATATGTTAAGTAACTGCC 1416
Qy 441 ProPro 442
Db 1417 CCACCT 1422

RESULT 13
US-09-630-940B-332
; Sequence 332, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
```

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-630-940B-332

Alignment Scores:
Pred. No.: 4,16e-229 Length: 2270
Score: 2185.00 Matches: 416
Percent Similarity: 94.80% Conservative: 3
Best Local Similarity: 94.12% Mismatches: 7
Query Match: 91.69% Indels: 16
DB: 4 Gaps: 1

US-09-670-568C-1 (1-448) x US-09-630-940B-332 (1-2270)
Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
Db 145 ATGTCCCAAGACACACAGACAAATGAATTCCTCAGTCCAGAGGTTTCCAGCATATCTGG 204
Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProlleAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGAACACGCTTATATGTTCAAGTTCAGCCCATTTGACTTGAACCTTTGTGATGAA 264
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 265 CCATCAGAGATGTTGCGACAAACAAGATTGAGATTAGCATGGACTGTATCCGCATGCAG 324
Qy 61 AspSerAspLeuSerAspProMetTrpProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTACCCCATGTGGCCACAGTACACGAACCTGGGGCTCTCTGAACAGC 384
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
Db 385 ATGACACAGCAGATTCAGAGGGCTCTCTGTCACCACTGCTCCCTATAACACAGACCACCGG 444
Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAACAGCGTCACGGCGCTCTCGCTTACGACAGCCAGCTCCACCTTCGATGCTCTC 504
Qy 121 SerProSerProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCAGCATCCCTCCAAACACAGCACTACCAGCCCGCCGACAGTTTCACCGTG 564
Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrThrTyrSerThrGluLeuLys 160
Db 565 TCCTTCCAGCAGTCGAGCAGCCCAAGTCGGCCACCTGGACGTATTCCTCACTGAACCTGAAG 624
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAATCTTACTGCCAATTTGCAAGACATGCCCATCCAGATCAAGTGTATGACCCCACT 684
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGGAGCTGTATCCGGGCCATGCTCTTACAAAAAAGCTGAGCAGCTCAGGAG 744
Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCCAAGCATGAGCTGAGCGGTGAATTCACAGGAGGACAGATTGCC 804
Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrValGluAspPro 240
Db 805 CTCTCTAGTCATTGTGATTGAGTAGAGGGGAACAGCCATGCCAGTATGTAAGATGCC 864
Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrGluPhe 260
Db 865 ATCAGAGGAGACAGAGTGTGTGTTATGAGCCACCCAGGTTGGCACTGAAATTC 924
Qy 261 ThrThrValLeuTyrAsnPheMetCysAsnSerCysValGlyGlyMetAsnArgArg 280
Db 925 ACGACAGCTTTGTACAAATTCATGTGTAACAGCAGTGTGTGTGGAGGGATGAACCGCGT 984
```

```
QY 281 ProileLeuileleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 985 CCAATTTTAAATCATGTTACTCTGGAAACCAGAGATGGGCAAGTCTCTGGGCCGACGCTGC 1044
QY 301 PheGluAlaArgileCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCCGGATCTGTGCTTCCCGAGGAAGACAGAGGAGCGGATGAAGATAGCATC 1104
QY 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAGCAGCAAGTTTCGGACATCAAGAACGGTGTATGGTACGAGCGCCGTTTCGT 1164
QY 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA 1224
QY 361 LeuLeuTyrlieuProValArgGlyArgGluThrTyrlieuMetLeuLeuLysLysGlu 380
Db 1225 CTGTTATACTTACCAGTGAGGGCCGCGAGACTTATGAAATGCTGTGAAGATCAAGAG 1284
QY 381 SerLeuGluLeuMetGlnTyrlieuProGlnHisThrIleGluThrTyrlieuArgGlnGln 400
Db 1285 TCCTCGAATCATGACGATACCTTCTCAGCACACAAATGAAACGTACAGGCAACAGCAA 1344
QY 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGCAGCAGCAGCTTACTTACAGAA----- 1374
QY 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1375 -----CAGACCTCAATACAGTCTCCATCTTCATATGTTAAGTAAACAGCTCC 1416
QY 441 ProPro 442
Db 1417 CCACCT 1422
RESULT 14
US-09-643-597-335
; Sequence 335, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-643-597-335
```

```
Alignment Scores:
Pred. No.: 1,46e-228 Length: 4849
Score: 2185.00 Matches: 416
Percent Similarity: 94.80% Conservative: 3
Best Local Similarity: 94.12% Mismatches: 7
Query Match: 91.69% Indels: 16
DB: 3 Gaps: 1
```

```
US-09-670-568c-1 (1-448) x US-09-643-597-335 (1-4849)
QY 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTTP 20
Db 145 ARGTCCTCCAGAGCACAGACAAATGAATTCCTCAGTCCAGAGGTTTTCAGACATATCTGG 204
QY 21 AspPheLeuGluGlnProileCysSerValGlnProileAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGAACAGCCATATATGTTTCAGTTCAGCCCATTCGACTTGAACATTTTGGATGAA 264
QY 41 ProSerGluAspGlyAlaThrAsnLysLysLysLysLysLysLysLysLysLysLysLys 60
Db 265 CCATCAGAAAGATGGTGGCAGACAAACAAAGATTGAGATTAGCATGCTATCCGATGCGAG 324
QY 61 AspSerAspLeuSerAspProMetTTPProGlnTyrlieuThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTCGGACCTGAGTGACCCCATGTGGCCACAGTACAGAACCTGGGGCTCTCTGAACAGC 384
QY 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrlieuThrAsnHisAla 100
Db 385 ATGGACACAGCAGATTTCAGAACGGCTCTCGTCCACAGTCCCTATAAACACAGACACGCG 444
QY 101 GlnAsnSerValThrAlaProSerProTyrlieuGlnProSerSerThrPheAspAlaLeu 120
Db 445 CAGAAACAGCGTCACGGCGCCCTCGCCCTACGACACAGCCAGCTCCACCTTCGATGCTCTC 504
QY 121 SerProSerProAlaIleProSerAsnThrAspTyrlieuProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCAGCGCATCCCTTCCAAACACCGACTACCCAGGCCCGCACAGTTTCGACG 564
QY 141 SerPheGlnGlnSerSerThrAlaLysSerAlaThrTyrlieuThrTyrlieuThrGluLeuLys 160
Db 565 TCCTTCAGACAGCTCGACACCGCCCAAGTCGGCCACTCGACCTATTCACCTGAACCTGAAG 624
QY 161 LysLeuTyrlieuCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
Db 625 AAACCTCTACTGCCAAATTCGAAAGACATGCCCATCCAGATCAAGGTGATGATGATGATGAT 684
QY 181 ProGlnGlyAlaValIleArgAlaMetProValTyrlieuLysLysAlaGluHisValThrGlu 200
Db 685 CCTCAGGAGCTGTGTTATCCGGCCCATGCTGTCTACAAAAAGCTGAGCAGCTCAGCGAG 744
QY 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
Db 745 GTGGTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCACAGGAGGACAGATTGCC 804
QY 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnTyrlieuValGluAspPro 240
Db 805 CCTCTAGTCTATTTGATTCGAGTAGAGGGGAACAGCCATGCCCATGTATGTAGAAGATGCC 864
QY 241 IleThrGlyArgGlnSerValIleuValProTyrlieuProGlnValGlyThrGluPhe 260
Db 865 ATCAGAGGAACAGAGTGTGCTGTATGAGCCACCCAGGTGGCTGACTGAATTC 924
QY 261 ThrThrValLeuTyrlieuAsnPheMetCysAsnSerSerCysValGlyMetAsnArgArg 280
Db 925 ACGACAGCTCTGTACAAATTCATGTGTAAACAGCAGTGTGTGGAGGGATGAACCCCGCT 984
QY 281 ProIleLeuIleIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys 300
Db 985 CCAATTTTAAATCATGTTTACTCTCGAAACACAGAGATGGGCAAGTCTCTGGGCCGACGCTC 1044
QY 301 PheGluAlaArgileCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db 1045 TTTGAGGCCCGGATCTGTGCTTCCCGAGGAAGACAGAGGAGCGGATGAAGATAGCATC 1104
QY 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
Db 1105 AGAAGCAGCAAGTTTCGGACATCAAGAACGGTGTATGGTACGAGCGCCGTTTCGT 1164
QY 341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
Db 1165 CAGAACACACATGGTATCCAGATGACATCCATCAAGAAACGAAGATCCCCAGATGATGAA 1224
```



```

Qy 361 LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuLysLeuGlu 380
Db 1225 CTGTTATACCTACCAGTCAGGGCGGTGAGACTTATGAAATGCTGTTGAAGATCAAAGAG 1384
Qy 381 SerLeuLeuLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGln 400
Db 1285 TCCCTGGAACCTCATGCGAGTACCTTCCCTCAGCACACAATTGAAACGTACAGGCAACAGCAA 1344
Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysHisLeuLeuSerAlaCysPheArgAsnGlu 420
Db 1345 CAGCAGCAGACACGACACTTACTTCAGAAA----- 1374
Qy 421 LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
Db 1375 -----CAGACCTCAATACAGTCTCCATCTTCATATGGTAAACAGCTCC 1416
Qy 441 ProPro 442
Db 1417 CCACCT 1422

RESULT 15
US-09-542-615A-335
; Sequence 335, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hoeken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 21021.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 4849
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-335

Alignment Scores:
Pred. No.: 1.46e-228 Length: 4849
Score: 2185.00 Matches: 416
Percent Similarity: 94.80% Conservative: 3
Best Local Similarity: 94.12% Mismatches: 7
Query Match: 91.69% Indels: 16
DB: Gaps: 1

US-09-670-568C-1 (1-448) x US-09-542-615A-335 (1-4849)
Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTyr 20
Db 145 ATGTCCAGAGCACACAGACAAATGAATTCCTCAGTCAGAGGTTTCCAGCATATCTGG 204
Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
Db 205 GATTTTCTGGAACAGCCTATATGTTTCAGTTCAGGCCCATTCGACTTGAACCTTTGGATGAA 264
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 265 CCATCAGAAGATGTGTGGCACAACAAAGATTGAGATTAGCATGGACTGTATCCCGCATGCAG 324
Qy 61 AspSerAspLeuSerAspProMetTyrProGlnTyrThrAsnLeuGlyLeuLeuAsnSer 80
Db 325 GACTTCGGACCTTGAGTGACCCCATGTGGCCACAGTACACGAACCTGGGGCTCTCTGAACAGC 384
Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerThrSerProTyrAsnThrAspHisAla 100

```

Search completed: October 3, 2005, 06:06:48
Job time : 283 secs